

From: Page, Thurman
Sent: Friday, June 18, 2004 2:31 PM
To: STIC-Biotech/ChemLib
Cc: Basi, Nirmal; Page, Thurman
Subject: FW: Rush sequence esrch for App No. 09/429,832 (use squence listing in parent 08/906,365case to do the search)

TWO MONTH AMENDMENT: RUSH SEARCH APPROVED

Thurman K. Page
SPE Art Units 1615 & 1616
Technology Center 1600

-----Original Message-----

From: Basi, Nirmal
Sent: Friday, June 18, 2004 1:21 PM
To: Page, Thurman
Subject: FW: Rush sequence esrch for App No. 09/429,832 (use squence listing in parent 08/906,365case to do the search)

Thurman, Cristina is out of the office, could you approve a rush search please.

-----Original Message-----

From: Basi, Nirmal
Sent: Friday, June 18, 2004 1:18 PM
To: Chan, Christina
Subject: Rush sequence esrch for App No. 09/429,832 (use squence listing in parent 08/906,365case to do the search)

Christina I am seeking approval for a RUSH sequence search, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi
Art Unit 1646
Office: Remsen Building, Room 4D68
Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 09/429,832 (please use the sequence listing in parent application 08/906,365 to do the search)

Result format: Paper.

Title NOVEL HUMAN ESTROGEN RECEPTOR-BETA
Inventors: BHAT, RAMESH A. et al

Priority Date: 8/5/97

Please search:

i) SEQ ID NO:2

RECEIVED
JUN 18 2004
STIC

Searcher: Jan
Phone: 72504
Location: _____
Date Picked Up: 6/20
Date Completed: 6/20
Searcher Prep/Review: _____
Clerical: 10
Online time: 10

TYPE OF SEARCH:

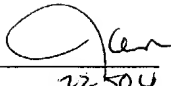
NA Sequences: _____
AA Sequences: ✓
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: ✓
WWW/Internet: _____
Other (specify): _____

Search commercial, issued and interference databases.

Thanks,
Nirmal S. Basi

Searcher: 
Phone: 22504
Location: _____
Date Picked Up: 4/20
Date Completed: 6/20
Searcher Prep/Review: _____
Clerical: 10
Online time: 60

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: ☒
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: ☒
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2004, 10:38:43 ; Search time 49 Seconds
(without alignments)
3053.597 Million cell updates/sec

Title: US-08-906-365-2
Perfect score: 2805
Sequence: 1 MDIKNSPSSLSNPSSTNSQ.....ECSPAEDSKSKSGSQWPSQ 530

Scoring table: BLOSUM62
Gapo9 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

ALIGNMENTS

RESULT 1
US-10-198-785-2
Sequence 2, Application US/10198785
Publication No. US20030022224A1
GENERAL INFORMATION:
APPLICANT: OLYMPUS OPTICAL CO., LTD.
TITLE OF INVENTION: Method of detecting binding reaction between protein and test su
FILE REFERENCE: 7E1-02S0538
CURRENT APPLICATION NUMBER: US/10/198,785
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: JP/2001-220444
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: JP/2001-221963
PRIOR FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 530
TYPE: PRT
ORGANISM: Homo sapiens
US-10-198-785-2

Query Match 100.0%; Score 2805; DB 14; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.1e-254;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSSTNSQSLPLEHGSIIYPSYVDSHHYPAWTFYSPAVMYSIPS 60
Db 1 MDIKNSPSSLSNPSSTNSQSLPLEHGSIIYPSYVDSHHYPAWTFYSPAVMYSIPS 60

QY 61 NVTNLEGGPGROTTSPNVLMPTPGHLSPLVVRQLSHLYAEQKSPWCSEARSLEHTLPVN 120
Db 61 NVTNLEGGPGROTTSPNVLMPTPGHLSPLVVRQLSHLYAEQKSPWCSEARSLEHTLPVN 120

QY 121 RETLKRKVSNGRCASFTVTPGSKRDAHFCAVCSDVASGHYGVNCSCEGKAFKRSIQGH 180
Db 121 RETLKRKVSNGRCASFTVTPGSKRDAHFCAVCSDVASGHYGVNCSCEGKAFKRSIQGH 180

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 2805 | 100.0 | 530 | 14 | US-10-198-785-2 |
| 2 | 2805 | 100.0 | 530 | 14 | US-10-157-031-106 |
| 3 | 2805 | 100.0 | 530 | 14 | US-10-392-274-4 |
| 4 | 2554 | 91.1 | 485 | 14 | US-10-278-481-3 |
| 5 | 2476.5 | 88.3 | 555 | 14 | US-10-373-271-1 |
| 6 | 2291 | 81.7 | 485 | 14 | US-10-278-481-2 |
| 7 | 2286 | 81.5 | 484 | 14 | US-10-278-481-13 |
| 8 | 2267 | 80.8 | 485 | 14 | US-10-278-481-5 |
| 9 | 2262 | 80.6 | 484 | 14 | US-10-278-481-14 |
| 10 | 2017 | 71.9 | 384 | 14 | US-10-278-481-15 |
| 11 | 1235.5 | 44.0 | 595 | 15 | US-10-148-835-5 |
| 12 | 1233.5 | 44.0 | 595 | 9 | US-09-853-033-2 |
| 13 | 1233.5 | 44.0 | 595 | 15 | US-10-148-835-1 |
| 14 | 1233.5 | 44.0 | 595 | 15 | US-10-148-835-2 |
| 15 | 1233.5 | 44.0 | 595 | 15 | US-10-148-835-9 |

QY 181 NDYICPATNCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRRCGYRLVRRORSADQLH 240
 DB 181 NDYICPATNCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRRCGYRLVRRORSADQLH 240
 QY 241 CAGKAKSGGHAPRVRELLDALSPEQLVLTLLAEPPHVLISRPSAPFTASMMSLTK 300
 DB 241 CAGKAKSGGHAPRVRELLDALSPEQLVLTLLAEPPHVLISRPSAPFTASMMSLTK 300
 QY 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWRSDHPGKLIAPDL 360
 DB 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWRSDHPGKLIAPDL 360
 QY 361 VLDRDEGKCVGEILEIFDMLLNTSRRELKLOHKEYLVCVKAMILLNSSMYPVLTATODA 420
 DB 361 VLDRDEGKCVGEILEIFDMLLNTSRRELKLOHKEYLVCVKAMILLNSSMYPVLTATODA 420
 QY 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLLSHVHASNKGMEHLNKK 480
 DB 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLLSHVHASNKGMEHLNKK 480
 QY 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSO 530
 DB 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSO 530

RESULT 2

US-10-157-031-106

; Sequence 106, Application US/10157031

; Publication No. US2003010890A1

; GENERAL INFORMATION:

; APPLICANT: Baranova, A. V.

; APPLICANT: Yankovsky, N. K.

; APPLICANT: Kozlov, A. P.

; APPLICANT: Lobahev, A. V.

; APPLICANT: Krukovskaya, L. L.

; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences

; FILE REFERENCE: 2760-103

; CURRENT APPLICATION NUMBER: US/10/157,031

; CURRENT FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 415

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 106

; LENGTH: 530

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-157-031-106

Query Match 100.0%; Score 2805; DB 14; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.1e-254;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSYNSCSQSIPLHSGSIYIPSSYVDSHHYPAWTFYSPAVMYSIPS 60
 DB 1 MDIKNSPSSLSNPSYNSCSQSIPLHSGSIYIPSSYVDSHHYPAWTFYSPAVMYSIPS 60

QY 61 NVTNLEGGPGROTTSPNVLPTPGHLSPLVVRHQLSHLYAEPOKSPWCARSLEHTLPVN 120
 DB 61 NVTNLEGGPGROTTSPNVLPTPGHLSPLVVRHQLSHLYAEPOKSPWCARSLEHTLPVN 120

QY 121 RETLKRKVSNGRCASPTVTPGSKRDAHFCAVCSDYASGYHYGVMSCEGCKAFKRSIQGH 180
 DB 121 RETLKRKVSNGRCASPTVTPGSKRDAHFCAVCSDYASGYHYGVMSCEGCKAFKRSIQGH 180

QY 181 NDYICPATNCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRRCGYRLVRRORSADQLH 240
 DB 181 NDYICPATNCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRRCGYRLVRRORSADQLH 240

QY 241 CAGKAKSGGHAPRVRELLDALSPEQLVLTLLAEPPHVLISRPSAPFTASMMSLTK 300
 DB 241 CAGKAKSGGHAPRVRELLDALSPEQLVLTLLAEPPHVLISRPSAPFTASMMSLTK 300

QY 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWRSDHPGKLIAPDL 360
 DB 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWRSDHPGKLIAPDL 360

DB 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWRSDHPGKLIAPDL 360
 QY 361 VLDRDEGKCVGEILEIFDMLLNTSRRELKLOHKEYLVCVKAMILLNSSMYPVLTATODA 420
 DB 361 VLDRDEGKCVGEILEIFDMLLNTSRRELKLOHKEYLVCVKAMILLNSSMYPVLTATODA 420
 QY 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLLSHVHASNKGMEHLNKK 480
 DB 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLLSHVHASNKGMEHLNKK 480
 QY 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSO 530
 DB 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSO 530

RESULT 3

US-10-392-274-4

; Sequence 4, Application US/10392274

; Publication No. US20030199472A1

; GENERAL INFORMATION:

; APPLICANT: AL-HENDY, AYMAN

; APPLICANT: LEE, EUN JIG

; APPLICANT: JAMESON, J. LARRY

; TITLE OF INVENTION: ADENOVIRUS-MEDIATED THERAPY FOR UTERINE FIBROIDS

; FILE REFERENCE: UTSG:252USPI

; CURRENT APPLICATION NUMBER: US/10/392,274

; CURRENT FILING DATE: 2003-03-19

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 530

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-392-274-4

Query Match 100.0%; Score 2805; DB 14; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.1e-254;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSYNSCSQSIPLHSGSIYIPSSYVDSHHYPAWTFYSPAVMYSIPS 60
 DB 1 MDIKNSPSSLSNPSYNSCSQSIPLHSGSIYIPSSYVDSHHYPAWTFYSPAVMYSIPS 60

QY 61 NVTNLEGGPGROTTSPNVLPTPGHLSPLVVRHQLSHLYAEPOKSPWCARSLEHTLPVN 120
 DB 61 NVTNLEGGPGROTTSPNVLPTPGHLSPLVVRHQLSHLYAEPOKSPWCARSLEHTLPVN 120

QY 121 RETLKRKVSNGRCASPTVTPGSKRDAHFCAVCSDYASGYHYGVMSCEGCKAFKRSIQGH 180
 DB 121 RETLKRKVSNGRCASPTVTPGSKRDAHFCAVCSDYASGYHYGVMSCEGCKAFKRSIQGH 180

QY 181 NDYICPATNCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRRCGYRLVRRORSADQLH 240
 DB 181 NDYICPATNCTIDKNRRKSCQACRLKCYEYGVWVKCGSRRRCGYRLVRRORSADQLH 240

QY 241 CAGKAKSGGHAPRVRELLDALSPEQLVLTLLAEPPHVLISRPSAPFTASMMSLTK 300
 DB 241 CAGKAKSGGHAPRVRELLDALSPEQLVLTLLAEPPHVLISRPSAPFTASMMSLTK 300

QY 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWRSDHPGKLIAPDL 360
 DB 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWRSDHPGKLIAPDL 360

QY 361 VLDRDEGKCVGEILEIFDMLLNTSRRELKLOHKEYLVCVKAMILLNSSMYPVLTATODA 420
 DB 361 VLDRDEGKCVGEILEIFDMLLNTSRRELKLOHKEYLVCVKAMILLNSSMYPVLTATODA 420

QY 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLLSHVHASNKGMEHLNKK 480
 DB 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQSQSMRLANLLMLLSHVHASNKGMEHLNKK 480

QY 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSO 530
 DB 481 CKNVVPVYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSO 530

Db 481 CKNVVFPYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSPQSQ 530

RESULT 4

US-10-278-481-3

Sequence 3, Application US/10278481

Publication No. US20030113803A1

GENERAL INFORMATION:

APPLICANT: K&O BIO AB

TITLE OF INVENTION: Orphan receptor

NUMBER OF SEQUENCES: 19

STREET: c/o Center for Biotechnology and Department of Medical Nutrition, Karolinska Institute

CITY: Huddinge

COUNTRY: Sweden

ZIP: S-14186

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,481

FILING DATE: 23-Oct-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/333,057

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/836,620

FILING DATE: <Unknown>

APPLICATION NUMBER: GB 9518272.1

FILING DATE: 08-SEP-1995

APPLICATION NUMBER: GB 9605550.4

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: GB 9607532.0

FILING DATE: 11-APR-1996

APPLICATION NUMBER: GB 9609576.5

FILING DATE: 08-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: GUSTAFSSON, Jan-Ake

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 485 amino acids

TYPE: amino acid

TOPOLOGY: linear

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-278-481-3

Query Match 91.1%; Score 2554; DB 14; Length 485;

Best Local Similarity 99.8%; Pred. No. 7.2e-231;

Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 46 MTFYSPAVMYSIPSNVTLNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPOKS 105

Db 1 MTFYSPAVMYSIPSNVTLNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPOKS 60

Qy 106 PWCARSLEHTLPVNRRLTKRVSGNRCASPVTPGSGKRDHFCVCSVDYASGYHYGWS 165

Db 61 PWCARSLEHTLPVNRRLTKRVSGNRCASPVTPGSGKRDHFCVCSVDYASGYHYGWS 120

Qy 166 CEGCKAFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVNWKCGSRRRCG 225

Db 121 CEGCKAFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVNWKCGSRRRCG 180

Qy 226 YRLVRQRSADQLHCAGKAKSGGHAPRVRELLDALSPPQLVTLLEAPPVHLISRP 285

Db 181 YRLVRQRSADQLHCAGKAKSGGHAPRVRELLDALSPPQLVTLLEAPPVHLISRP 240

Qy 286 SAPFTEASMMSLTKLADKELVHMLSWAKKIPGFVELSLFDQVRLLESCKNVEVLMVGLMW 345

Db 241 SAPFTEASMMSLTKLADKELVHMLSWAKKIPGFVELSLFDQVRLLESCKNVEVLMVGLMW 300

Qy 346 RSIDHPGKLIAPADLVLRDDEGKCVGEILEIFDMLLATTSRFRELKLOHKEYLCVKAMIL 405

Db 301 RSIDHPGKLIAPADLVLRDDEGKCVGEILEIFDMLLATTSRFRELKLOHKEYLCVKAMIL 360

Qy 406 LNNSMYPLVTATQDADSRKLAHLINAVTDALVVIAGSGISSQQOSMELANLLMLLSHV 465

Db 361 LNNSMYPLVTATQDADSRKLAHLINAVTDALVVIAGSGISSQQOSMELANLLMLLSHV 420

Qy 466 RHASNKGEHLLNMKCKQNVFPYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSO 525

Db 421 RHASNKGEHLLNMKCKQNVFPYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSO 480

Qy 526 NPQSQ 530

Db 481 NLQSQ 485

RESULT 5

US-10-373-271-1

Sequence 1, Application US/10373271

Publication No. US20030162257A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Quinet, Elaine M.

APPLICANT: Pan, Ermei

TITLE OF INVENTION: Nucleic Acid Molecule Encoding a No. US20030162257A1e1 Estrogen

TITLE OF INVENTION: Variant

FILE REFERENCE: AM100361

CURRENT APPLICATION NUMBER: US/10/373,271

CURRENT FILING DATE: 2003-02-25

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.2

SEQ ID NO 1

LENGTH: 555

TYPE: PRT

ORGANISM: human testis

FEATURE:

NAME/KEY: misc feature

LOCATION: (534)..(534)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (542)..(545)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-373-271-1

Query Match 88.3%; Score 2476.5; DB 14; Length 555;

Best Local Similarity 92.4%; Pred. No. 1.7e-223;

Matches 477; Conservative 4; Mismatches 14; Indels 21; Gaps 3;

Qy 1 MDIKNSPSSLNSSPSSYNCSQSILPLEHSGSIYIPSSYVDSHSHYEPAMTFYSPAVMYSIPS 60

Db 11 MNKNSPSSLNSSPSSYNCSQSILPLEHSGSIYIPSSYVDSHSHYEPAMTFYSPAVMYSIPS 70

Qy 61 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPOKSPWCEARSLIHTLPVN 120

Db 71 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPOKSPWCEARSLIHTLPVN 130

Qy 121 RETLKRVSGNRCASPVTPGSGKRDHFCVCSVDYASGYHYGWSCEGCKAFKRSIQGH 180

Db 131 RETLKRVSGNRCASPVTPGSGKRDHFCVCSVDYASGYHYGWSCEGCKAFKRSIQGH 190

Qy 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEYGVNWKCGSRRRCGRLVRQRSADQLH 240

Db 191 NDYICPATNQCTIDKNRRKSCQACRLKCYEYGVNWKCGSRRRCGRLVRQRSADQLH 250

Qy 241 CAGKAKSGGHAPRVRELLDALSPPQLVTLLEAPPVHLISRPAPFTEASMMSLTK 300

Db 251 CAGKAKSGGHAPRVRELLDALSPPQLVTLLEAPPVHLISRPAPFTEASMMSLTK 310

Qy 301 LAKELVHMLSWAKKIPGFVELSLFDQVRLLESCKNVEVLMVGLMWSDHPGKLIAPADL 360

Db 311 LADKELVHMSWAKIPGFVELSLPDQVRLLESCHMEVLMGLMNRSIDHPGKLIAPDOL 370
 Qy 361 VLDRDGGKVEGLEIFDMLATTSSRFELKQHKYLCVKAMILLNSSMYPVLTATODA 420
 Db 371 VLDRDGGKVEGLEIFDMLATTSSRFELKQHKYLCVKAMILLNSSMYPVLTATODA 430
 Qy 421 DSSRKLHLINAVTDALVWVIAKSGISSQQSSMRLANLMLLSHVPHASNKGMHLLNMK 480
 Db 431 DSSRKLHLINAVTDALVWVIAKSGISSQQSSMRLANLMLLSHVPHAR----- 479
 Qy 481 CKNVVPPVYDILLLEMLNA--HVLRGCKSSITGSSCSP 514
 Db 480 -----LYIWLAKMFAALKOILRAPFS--SRCCFP 507

RESULT 6

US-10-278-481-2
 ; Sequence 2, Application US/10278481
 ; Publication No. US20030113803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KARO BIO AB
 ; TITLE OF INVENTION: Orphan receptor
 ; NUMBER OF SEQUENCES: 19
 ; STREET: c/o Center for Biotechnology and Department
 ; of Medical Nutrition, Karolinska Nutrition, Karolinska
 ; Institute
 ; CITY: Huddinge
 ; COUNTRY: Sweden
 ; ZIP: S-14186
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/278,481
 ; FILING DATE: 23-Oct-2002
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/333,057
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/836,620
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: GB 9518272.1
 ; FILING DATE: 08-SEP-1995
 ; APPLICATION NUMBER: GB 9605550.4
 ; FILING DATE: 15-MAR-1996
 ; APPLICATION NUMBER: GB 9607532.0
 ; FILING DATE: 11-APR-1996
 ; APPLICATION NUMBER: GB 9609576.5
 ; FILING DATE: 08-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GUSTAFSSON, Jan-Ake
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 485 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; ORGANISM: Rattus rattus
 ; ORIGINAL SOURCE:
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-278-481-2

Query Match 81.7%; Score 2291; DB 14; Length 485;
 Best Local Similarity 88.7%; Pred. No. 3.8e-206;
 Matches 430; Conservative 23; Mismatches 32; Indels 0; Gaps 0;
 Qy 46 MTFYSPAVMNYISNVNTEGGPGROTTSNVLWPTPGHLSPVLVHRQLSHLYAEPOKS 105
 Db 1 MTFYSPAVMNYSVRGTSINLDDGGPVLSTSNVLWPTSGHLSPLATHCQSSLYAEPOKS 60
 Qy 106 PWCARSLEHTLPVNRRETLKPKKGNRCASPVTCGSKRDAHFCVACSDYASGHYGVWS 165
 Db 61 PWCARSLEHTLPVNRRETLKPKKSGSCASPVTSNPKRDAHFCVACSDYASGHYGVWS 120

Qy 166 CEGCKAPFKRSIQGHNDYICPATNOCTIDKVRKSCQAQLRKCYEVGMVKGSRERCG 225
 Db 121 CEGCKAPFKRSIQGHNDYICPATNOCTIDKVRKSCQAQLRKCYEVGMVKGSRERCG 180
 Qy 226 YRLVROBSADQLHCAKAKXSGHAPRVRELLLDALSPQLVLTLEAPPVHLISRP 285
 Db 181 YRLVROBSADQLHCAKAKXSGHAPRVRELLLDALSPQLVLTLEAPPVHLISRP 240
 Qy 286 SAPPTASMMMSLTKLADKBLVHMSWAKIPGFVELSLPDQVRLLESCHMEVLMGLMW 345
 Db 241 SMPPTASMMMSLTKLADKBLVHMSWAKIPGFVELSLPDQVRLLESCHMEVLMGLMW 300
 Qy 346 RSIDHPGKLIAPDVLDRDGGKVEGLEIFDMLATTSSRFELKQHKYLCVKAMIL 405
 Db 301 RSIDHPGKLIAPDVLDRDGGKVEGLEIFDMLATTSSRFELKQHKYLCVKAMIL 360
 Qy 406 LNNSMYPVLTATQDADSSRKLHLINAVTDALVWVIAKSGISSQQSSMRLANLMLLSHV 465
 Db 361 LNNSMYPVLTATQDADSSRKLHLINAVTDALVWVIAKSGISSQQSSMRLANLMLLSHV 420
 Qy 466 RHASNKGMHLLNMKCKNVVPPVYDILLLEMLNAHVLRGCKSSITGSSCSPADSKSGSQ 525
 Db 421 RHASNKGMHLLNMKCKNVVPPVYDILLLEMLNAHVLRGCKSSITGSSCSPADSKSGSQ 480
 Qy 526 NPQSQ 530
 Db 481 NLQSQ 485

RESULT 7

US-10-278-481-13
 ; Sequence 13, Application US/10278481
 ; Publication No. US20030113803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KARO BIO AB
 ; TITLE OF INVENTION: Orphan receptor
 ; NUMBER OF SEQUENCES: 19
 ; STREET: c/o Center for Biotechnology and Department
 ; of Medical Nutrition, Karolinska Nutrition, Karolinska
 ; Institute
 ; CITY: Huddinge
 ; COUNTRY: Sweden
 ; ZIP: S-14186
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/278,481
 ; FILING DATE: 23-Oct-2002
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/333,057
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/836,620
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: GB 9518272.1
 ; FILING DATE: 08-SEP-1995
 ; APPLICATION NUMBER: GB 9605550.4
 ; FILING DATE: 15-MAR-1996
 ; APPLICATION NUMBER: GB 9607532.0
 ; FILING DATE: 11-APR-1996
 ; APPLICATION NUMBER: GB 9609576.5
 ; FILING DATE: 08-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GUSTAFSSON, Jan-Ake
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 484 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; ORIGINAL SOURCE:

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; ORGANISM: Rattus rattus
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-278-481-13

Query Match      81.5%; Score 2286; DB 14; Length 484;
Best Local Similarity 88.6%; Pred. No. 1.1e-205;
Matches 429; Conservative 23; Mismatches 32; Indels 0; Gaps 0;

Qy 46 MTFYSPAVMYVSIPIGNTVNLGGPGROTTSPNVLWPTPGHLSPLVHRLSHLYAEPOKS 105
Db 1 MTFYSPAVMYVSIPIGNTVNLGGPGROTTSPNVLWPTPGHLSPLVHRLSHLYAEPOKS 60

Qy 106 PWCEARSLHTLPVNRRETLKRVGNRCASPVTPGSGKDAHFCVCSYASGYHYGWS 165
Db 61 PWCEARSLHTLPVNRRETLKRVGNRCASPVTPGSGKDAHFCVCSYASGYHYGWS 120

Qy 166 CEGKAFPKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVMVKCGSRRRCG 225
Db 121 CEGKAFPKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVMVKCGSRRRCG 180

Qy 226 YRLVRQRSADEQLHCAGKAKSGHAPRVRELLDALSPQLVLTLEAEPHVLISRP 285
Db 181 YRLVRQRSSSEVHCLSKAKNGGHAAPRVKELLSTLSPEQLVLTLEAEPHVLISRP 240

Qy 286 SAPTEASMMSLTKLADKELVHMSWAKKIPGFVELSLFDQVRLLESCHWVLMGLMW 345
Db 241 SMPTEASMMSLTKLADKELVHMGWAKKIPGFVELSLDQVRLLESCHWVLMGLMW 300

Qy 346 RSIDHPGKLIIFAPDLVLRDEGKCVGEILEIFDMLLATTSFRELKQKEYLVCVKMIL 405
Db 301 RSIDHPGKLIIFAPDLVLRDEGKCVGEILEIFDMLLATTSFRELKQKEYLVCVKMIL 360

Qy 406 LNSSMYPLVTATODASRKLHLNNAVTDALVWVIKSGISSQOOSRLANLLMLSHV 465
Db 361 LNSSMYPLASANOEAESSRKLTLLNNAVTDALVWVIKSGISSQOOSRLANLLMLSHV 420

Qy 466 RHASNKGHEHLNMMCKNVVPPYDILLLEMLNAHLRGCKSSITGSECSPAEDSKSKESQ 525
Db 421 RHISNKGHEHLNMMCKNVVPPYDILLLEMLNAHLRGCKSSITGSECSPAEDSKSKESQ 480

Qy 526 NPQS 529
Db 481 NLQS 484

RESULT 8
US-10-278-481-5
; Sequence 5, Application US/10278481
; Publication No. US20030113803A1
; GENERAL INFORMATION:
; APPLICANT: KARO BIO AB
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; STREET: c/o Center for Biotechnology and Department of Medical Nutrition, Karolinska Nutrition, Karolinska
; CITY: Huddinge
; COUNTRY: Sweden
; ZIP: S-14186
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,481
; FILING DATE: 23-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,057
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/836,620
; FILING DATE: <Unknown>
; APPLICATION NUMBER: GB 9518272.1

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; FILING DATE: 08-SEP-1995
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: GUSTAFSSON, Jan-Ake
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORGANISM: Mus musculus
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-278-481-5

Query Match      80.8%; Score 2267; DB 14; Length 485;
Best Local Similarity 88.0%; Pred. No. 6.8e-204;
Matches 427; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

Qy 46 MTFYSPAVMYVSIPIGNTVNLGGPGROTTSPNVLWPTPGHLSPLVHRLSHLYAEPOKS 105
Db 1 MAFYSPAVMYVSIPIGNTVNLGGPGROTTSPNVLWPTSGHLSPLATHCQSSLLYAEPOKS 60

Qy 106 PWCEARSLHTLPVNRRETLKRVGNRCASPVTPGSGKDAHFCVCSYASGYHYGWS 165
Db 61 PWCEARSLHTLPVNRRETLKRVGNRCASPVTPGSGKDAHFCVCSYASGYHYGWS 120

Qy 166 CEGKAFPKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVMVKCGSRRRCG 225
Db 121 CEGKAFPKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVMVKCGSRRRCG 180

Qy 226 YRLVRQRSADEQLHCAGKAKSGHAPRVRELLDALSPQLVLTLEAEPHVLISRP 285
Db 181 YRLVRQRSSSEVHCLSKAKNGGHAAPRVKELLSTLSPEQLVLTLEAEPHVLISRP 240

Qy 286 SAPTEASMMSLTKLADKELVHMSWAKKIPGFVELSLFDQVRLLESCHWVLMGLMW 345
Db 241 SMPTEASMMSLTKLADKELVHMGWAKKIPGFVELSLDQVRLLESCHWVLMGLMW 300

Qy 346 RSIDHPGKLIIFAPDLVLRDEGKCVGEILEIFDMLLATTSFRELKQKEYLVCVKMIL 405
Db 301 RSIDHPGKLIIFAPDLVLRDEGKCVGEILEIFDMLLATTSFRELKQKEYLVCVKMIL 360

Qy 406 LNSSMYPLVTATODASRKLHLNNAVTDALVWVIKSGISSQOOSRLANLLMLSHV 465
Db 361 LNSSMYPLASANOEAESSRKLTLLNNAVTDALVWVIKSGISSQOOSRLANLLMLSHV 420

Qy 466 RHASNKGHEHLNMMCKNVVPPYDILLLEMLNAHLRGCKSSITGSECSPAEDSKSKESQ 525
Db 421 RHISNKGHEHLNMMCKNVVPPYDILLLEMLNAHLRGCKSSITGSECSPAEDSKSKESQ 480

Qy 526 NPQS 530
Db 481 NLQS 485

RESULT 9
US-10-278-481-14
; Sequence 14, Application US/10278481
; Publication No. US20030113803A1
; GENERAL INFORMATION:
; APPLICANT: KARO BIO AB
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; STREET: c/o Center for Biotechnology and Department of Medical Nutrition, Karolinska Nutrition, Karolinska
; CITY: Huddinge
; COUNTRY: Sweden

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Sun Jun 20 11:32:41 2004

ZIP: S-14186
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,481
FILING DATE: 23-Oct-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,057
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/836,620
FILING DATE: <Unknown>
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: GUSTAFSSON, Jan-Ake
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-278-481-14

Query Match 80.6%; Score 2262; DB 14; Length 484;
Best Local Similarity 88.0%; Pred. No. 2e-203;
Matches 426; Conservative 23; Mismatches 35; Indels 0; Gaps 0;
QY 46 MTFSPAVMYSPISNVNTEGGPGRTPTSPVNLWPTGHLSPVVRQLSHLYAEPQKS 105
DB 1 MAFVSPAVMYSPVSSVTEGGPGVQTASPNVLPWPTSGHLSPLATHCQSSLLYAEQKS 60
QY 106 PWCARSLEHTLPVNRRTLRKRVSGNRCASPVTPGSKRDRAHCAVCSYASGYHYGWS 165
DB 61 PWCARSLEHTLPVNRRTLRKRVSGNRCASPVTPGSKRDRAHCAVCSYASGYHYGWS 120
QY 166 CEGKAFKRSIQGHNDYICPATNOCTIDKNRRKSCQACRLKCYEVMVKCGSRRCG 225
DB 121 CEGKAFKRSIQGHNDYICPATNOCTIDKNRRKSCQACRLKCYEVMVKCGSRRCG 180
QY 226 YRLVRRQRSADQLHCAGKARSGCHAPRVRELLDALSPEQLVLTLLAEPPHVLISRP 285
DB 181 YRLVRRQRSADQLHCAGKARSGCHAPRVRELLDALSPEQLVLTLLAEPPHVLISRP 240
QY 286 SAPTEASMMWLTUKLADKELVHMISWAKKIPGVFELSFDQVRLLESQWVLMVGLMW 345
DB 241 SMPTEASMMWLTUKLADKELVHMISWAKKIPGVFELSFDQVRLLESQWVLMVGLMW 300
QY 346 RSIDHPGKLIAPADVLDRDEGKCVGEGILEIFDMLLATTSRFRELKIQHKEYLCVXAMIL 405
DB 301 RSIDHPGKLIAPADVLDRDEGKCVGEGILEIFDMLLATTSRFRELKIQHKEYLCVXAMIL 360
QY 406 LNSNMYPLVATQADSRKLAHLNNAVTLVWIAKSGISSQOQSMRLANMLLSHV 465
DB 361 LNSNMYPLVATQADSRKLAHLNNAVTLVWIAKSGISSQOQSMRLANMLLSHV 420
QY 466 RHASNKGMHLLNKKCNVPPVYDILLEMNAHLVLRGKSSITGSECSPAEDSKSKEGQ 525
DB 421 RHISNKGHEHLLSNKCNVPPVYDILLEMNAHLVLRGKSSITGSECSPAEDSKSKEGQ 480
QY 526 NPQS 529
DB 481 NLQS 484

RESULT 10
US-10-278-481-15
Sequence 15, Application US/10278481
Publication No. US20030113803A1
GENERAL INFORMATION:
APPLICANT: KARO BIO AB
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
STREET: c/o Center for Biotechnology and Department
of Medical Nutrition, Karolinska Nutrition, Karolinska
Institute
CITY: Huddinge
COUNTRY: Sweden
ZIP: S-14186
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,481
FILING DATE: 23-Oct-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,057
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/836,620
FILING DATE: <Unknown>
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: GUSTAFSSON, Jan-Ake
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-278-481-15

Query Match 71.9%; Score 2017; DB 14; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.5e-180;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86 LSPLVVRQLSHLYAEPQKSPWCARSLEHTLPVNRRTLRKRVSGNRCASPVTPGSKRD 145
DB 2 LSPLVVRQLSHLYAEPQKSPWCARSLEHTLPVNRRTLRKRVSGNRCASPVTPGSKRD 61
QY 146 AHFCVCSYASGYHYGWSCEGKAFKRSIQGHNDYICPATNOCTIDKNRRKSCQACR 205
DB 62 AHFCVCSYASGYHYGWSCEGKAFKRSIQGHNDYICPATNOCTIDKNRRKSCQACR 121
QY 206 LRKCYEVMVKCGSRRCGTYRLVRRQRSADQLHCAGKARSGCHAPRVRELLDALS 265
DB 122 LRKCYEVMVKCGSRRCGTYRLVRRQRSADQLHCAGKARSGCHAPRVRELLDALS 181
QY 266 EQVLVLTLLAEPPHVLISRPSPAPTEASMMWLTUKLADKELVHMISWAKKIPGVFELS 325
DB 182 EQVLVLTLLAEPPHVLISRPSPAPTEASMMWLTUKLADKELVHMISWAKKIPGVFELS 241
QY 326 DOVRLLESQWVLMVGLMWVRSIDHPGKLIAPADVLDRDEGKCVGEGILEIFDMLLATTS 385
DB 242 DOVRLLESQWVLMVGLMWVRSIDHPGKLIAPADVLDRDEGKCVGEGILEIFDMLLATTS 301

QY 386 REFELKQHEVLCVAMILLNSMYPVLTATQDADSSRKLHLNAVTDALVWVIAKSG 445
 DB 302 REFELKQHEVLCVAMILLNSMYPVLTATQDADSSRKLHLNAVTDALVWVIAKSG 361
 QY 446 ISSQOOSRNLANLMLSHVRHA 468
 DB 362 ISSQOOSRNLANLMLSHVRHA 384
 RESULT 13
 US-10-148-835-5
 ; Sequence 5, Application US/10148835
 ; Publication No. US20030207380A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SAITO et al.
 ; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
 ; FILE REFERENCE: 2185-0648P
 ; CURRENT APPLICATION NUMBER: US/10/148,835
 ; CURRENT FILING DATE: 2002-10-11
 ; NUMBER OF SEQ ID NOS: 213
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 595
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-148-835-5

Query Match 44.0%; Score 1235.5; DB 15; Length 595;
 Best Local Similarity 48.4%; Pred. No. 8.2e-107;
 Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;
 QY 5 NSPSSINSPSSYNCOSILPLEH--GSTIYIPSS--YVDSHHEYPAMTFYSPAVMNVSIPT 60
 DB 21 NELEPLNR-----OLKIPLERPLGEVILDSKFAVYNYPEGAAYEFNAANAQAQVYG 74
 QY 61 NVTNLGGGPRQ-----TTSNVLWPTFGHLS-LVVRQLSHLYAE 101
 DB 75 Q-TGLPYGCGSEAAAFSGNLGFPPLNSVSPMLLHPPLSPFLPHQCHQVPPYILE 133
 QY 102 POKSPWC--EARSLEHTLPVNRETLKRKVGSRNCASPVYGPQ-----SKDHAFCVACSD 154
 DB 134 NEPSGYTVREAGPPAFYRP---NSDNRQGGRELRLASTNDKGSMAESAKETRYCAVND 190
 QY 155 YASGVHYGVWSCGCGKAPFKRSIOGHNDYICPATNCTIDKNRRKSCQACRLKCYEVM 214
 DB 191 YASGVHYGVWSCGCGKAPFKRSIOGHNDYICPATNCTIDKNRRKSCQACRLKCYEVM 250
 QY 215 VKGSRRRRCGVRLVRRORSADQLHCAGKAKRSGCHAPVR-----EL 258
 DB 251 MKGGIRKDRRGGMKXKQRDD-----GEGRGEVGSAGDMRAANLWPSPLMIKRSKNS 305
 QY 259 LLDALSPQLVLTLEAEPHVLISR--PSAPFTEASMMSLTKLADKELVHMIWAKKI 316
 DB 306 LALSUTADQMSALLDAEPP-ILYSEYDTPRPFSEASMMGLLTNLADRLVHMINWAKRV 364
 QY 317 PGFVELSLDQVRLLESCEMVEVLMMGLMWRSIDHPGKLI FAPDLVLDREDEGKCVGILBI 376
 DB 365 PGFVDLTLDQVHLLSCAWLEILMIGLVWRSVEHPGKLI FAPNLILDRNQKCVGMEVI 424
 QY 377 FMLLATTSRFRELKQHEVLCVAMILLNSMYPVLTATQDADSSRKLHLNAVTD 435
 DB 425 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRLDKITD 484
 QY 436 ALVWVIAKSGISSQOOSRNLANLMLSHVRHASKMGHEHLNLMKCNVVPVYDILLEM 495
 DB 485 TLHLWAKAGLTQQOQHQRALQALLILSHIRMSNKGHEHLYSMKCNVVPVYDILLEM 544
 QY 496 NAHVL 500
 DB 545 DAHRL 549

RESULT 12

US-09-853-033-2
 ; Sequence 2, Application US/09853033
 ; Patent No. US20020100068A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHAMON, PIERRE
 ; TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
 ; FILE REFERENCE: 065691/0222
 ; CURRENT APPLICATION NUMBER: US/09/853,033
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: FR 00/12570
 ; PRIOR FILING DATE: 2000-10-03
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 595
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-853-033-2

Query Match 44.0%; Score 1233.5; DB 9; Length 595;
 Best Local Similarity 48.4%; Pred. No. 1.3e-106;
 Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;
 QY 5 NSPSSINSPSSYNCOSILPLEH--GSTIYIPSS--YVDSHHEYPAMTFYSPAVMNVSIPT 60
 DB 21 NELEPLNR-----OLKIPLERPLGEVILDSKFAVYNYPEGAAYEFNAANAQAQVYG 74
 QY 61 NVTNLGGGPRQ-----TTSNVLWPTFGHLS-LVVRQLSHLYAE 101
 DB 75 Q-TGLPYGCGSEAAAFSGNLGFPPLNSVSPMLLHPPLSPFLPHQCHQVPPYILE 133
 QY 102 POKSPWC--EARSLEHTLPVNRETLKRKVGSRNCASPVYGPQ-----SKDHAFCVACSD 154
 DB 134 NEPSGYTVREAGPPAFYRP---NSDNRQGGRELRLASTNDKGSMAESAKETRYCAVND 190
 QY 155 YASGVHYGVWSCGCGKAPFKRSIOGHNDYICPATNCTIDKNRRKSCQACRLKCYEVM 214
 DB 191 YASGVHYGVWSCGCGKAPFKRSIOGHNDYICPATNCTIDKNRRKSCQACRLKCYEVM 250
 QY 215 VKGSRRRRCGVRLVRRORSADQLHCAGKAKRSGCHAPVR-----EL 258
 DB 251 MKGGIRKDRRGGMKXKQRDD-----GEGRGEVGSAGDMRAANLWPSPLMIKRSKNS 305
 QY 259 LLDALSPQLVLTLEAEPHVLISR--PSAPFTEASMMSLTKLADKELVHMIWAKKI 316
 DB 306 LALSUTADQMSALLDAEPP-ILYSEYDTPRPFSEASMMGLLTNLADRLVHMINWAKRV 364
 QY 317 PGFVELSLDQVRLLESCEMVEVLMMGLMWRSIDHPGKLI FAPDLVLDREDEGKCVGILBI 376
 DB 365 PGFVDLTLDQVHLLSCAWLEILMIGLVWRSVEHPGKLI FAPNLILDRNQKCVGMEVI 424
 QY 377 FMLLATTSRFRELKQHEVLCVAMILLNSMYPVLTATQDADSSRKLHLNAVTD 435
 DB 425 FDMLLATSRFRMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRLDKITD 484
 QY 436 ALVWVIAKSGISSQOOSRNLANLMLSHVRHASKMGHEHLNLMKCNVVPVYDILLEM 495
 DB 485 TLHLWAKAGLTQQOQHQRALQALLILSHIRMSNKGHEHLYSMKCNVVPVYDILLEM 544
 QY 496 NAHVL 500
 DB 545 DAHRL 549

RESULT 13
 US-10-148-835-1
 ; Sequence 1, Application US/10148835
 ; Publication No. US20030207380A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SAITO et al.
 ; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION

```

; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-1

Query Match      44.0%; Score 1233.5; DB 15; Length 595;
Best Local Similarity 48.4%; Pred. No. 1.3e-106;
Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;

QY 5 NSPSSLNSPSSVNCQSILPLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAVMYSIPS 60
Db 21 NELEPLNRP-----OLKIPLERPLGEVYLDSSKPAVYNYPEGAAYEFNAAAAAQAQVYG 74
QY 61 NVTNLEGGPGRQ-----TTSFNVLMPTPGHLSPL-LVVHRLSHLYAE 101
Db 75 Q-TGLPYGPGSEAAAFSGNSGLGFPPLNSVSPPLMLLHPPLQSPPLQPHGQOVPYYLE 133
QY 102 POKSPMC--EARSLEHTLPVNRRETLKRVKSGNRCASPVTPG-----SKDAHFCAVCS 154
Db 134 NEPSGYTVREAGPPAFYRP---NSDNRQGRERLASTNDKGSMAESAKETRYCAVCND 190
QY 155 YASGYHYGVMSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVGM 214
Db 191 YASGYHYGVMSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVGM 250
QY 215 VKGSRERRCYRLVRRQSRASDLHCAGKAKRSKGHAPRV-----REL 258
Db 251 MKGGIRKDRGGRLMKHKRQDD-----GEGRGEVGSAGDMRAANLWPSPLMIKRSKNS 305
QY 259 LLDALSPQVLTLLEAEPPHYLISR--PSAPPTTEASMMMLTKLADKELVHMISWAKKI 316
Db 306 LALSLTADQVMSALIDAEP--ILYSEYDPTRPFSSEASMMGLLTNLADRELHVHMINWAKRV 364
QY 317 PGFVELSIFDOVRLLESCHWEVLMMGLMWSIDHPGKLIPAPDLVLDROGKCVGEILEI 376
Db 365 PGFVDLTLDQVHLLHCANWLEILMGLVWRSMEHPGKLLFAPNLLLDROGKCVGEVVEI 424
QY 377 FDMLLATTSRPRELKLQHKYLCVKAMILLNSMYPVLTAT-QDADSSRKLALHNAVTD 435
Db 425 FDMLLATTSRFRMNLQGEFVCLKSIILNSGVYTFSLSTLSLEEKDHIHRLDKITD 484
QY 436 ALVWVIKSGISSQOOSMRLANILMLLSHVHSHASNKGEHLNKKCNVVPVYDILLLEML 495
Db 485 TLILHMAKAGLTQQOQHRLAQLLLTLSHIRHNSKNKGHEHLYSMCKKNVVPYDILLLEML 544
QY 496 NAHVL 500
Db 545 DAHRL 549

RESULT 15
US-10-148-835-9
; Sequence 9, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-9

Query Match      44.0%; Score 1233.5; DB 15; Length 595;
Best Local Similarity 48.4%; Pred. No. 1.3e-106;
Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;

QY 5 NSPSSLNSPSSVNCQSILPLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAVMYSIPS 60
Db 21 NELEPLNRP-----OLKIPLERPLGEVYLDSSKPAVYNYPEGAAYEFNAAAAAQAQVYG 74
QY 61 NVTNLEGGPGRQ-----TTSFNVLMPTPGHLSPL-LVVHRLSHLYAE 101
Db 75 Q-TGLPYGPGSEAAAFSGNSGLGFPPLNSVSPPLMLLHPPLQSPPLQPHGQOVPYYLE 133
QY 102 POKSPMC--EARSLEHTLPVNRRETLKRVKSGNRCASPVTPG-----SKDAHFCAVCS 154
Db 134 NEPSGYTVREAGPPAFYRP---NSDNRQGRERLASTNDKGSMAESAKETRYCAVCND 190
QY 155 YASGYHYGVMSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVGM 214
Db 191 YASGYHYGVMSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVGM 250
QY 215 VKGSRERRCYRLVRRQSRASDLHCAGKAKRSKGHAPRV-----EL 258
Db 251 MKGGIRKDRGGRLMKHKRQDD-----GEGRGEVGSAGDMRAANLWPSPLMIKRSKNS 305
QY 259 LLDALSPQVLTLLEAEPPHYLISR--PSAPPTTEASMMMLTKLADKELVHMISWAKKI 316
Db 306 LALSLTADQVMSALIDAEP--ILYSEYDPTRPFSSEASMMGLLTNLADRELHVHMINWAKRV 364
QY 317 PGFVELSIFDOVRLLESCHWEVLMMGLMWSIDHPGKLIPAPDLVLDROGKCVGEILEI 376
Db 365 PGFVDLTLDQVHLLHCANWLEILMGLVWRSMEHPGKLLFAPNLLLDROGKCVGEVVEI 424
QY 377 FDMLLATTSRPRELKLQHKYLCVKAMILLNSMYPVLTAT-QDADSSRKLALHNAVTD 435
Db 425 FDMLLATTSRFRMNLQGEFVCLKSIILNSGVYTFSLSTLSLEEKDHIHRLDKITD 484
QY 436 ALVWVIKSGISSQOOSMRLANILMLLSHVHSHASNKGEHLNKKCNVVPVYDILLLEML 495
Db 485 TLILHMAKAGLTQQOQHRLAQLLLTLSHIRHNSKNKGHEHLYSMCKKNVVPYDILLLEML 544
QY 496 NAHVL 500
Db 545 DAHRL 549

RESULT 14
US-10-148-835-2
; Sequence 2, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-2
```

| | | | |
|----|-----|---|-----|
| Db | 75 | Q-TGLPYGSGEAAAFNGNLGGFPPLNSVSPPLMLLHPPQLSPFFLOPHGQQQVYYLE | 133 |
| Qy | 102 | PKSEWC--EARSLEHTLTVNRRETLKRVSGNRKASPVYTGPG-----SKRDAHFCVACSD | 154 |
| Db | 134 | NEPSGYTVREAGPPAFYRP---NSDNRRQGGRERLASTNDKSGMAMESAKETRYCAVCND | 190 |
| Qy | 155 | YASGYHYGWSCEGCKAFKRSIOGHNDYICPATNOCCTIDKNRRKSCQACRLKCYEYGM | 214 |
| Db | 191 | YASGYHYGWSCEGCKAFKRSIOGHNDYICPATNOCCTIDKNRRKSCQACRLKCYEYGM | 250 |
| Qy | 215 | VKGSRRRCGYRLVRRORSADQLHFCAGKAKRSGGHAPVR-----EL | 258 |
| Db | 251 | MKGGRKDRRGGRMLKHKKQRDD-----GEGRGEVGSAGDMAANLWSPPLMIKESKNS | 305 |
| Qy | 259 | LLDALSPQLVLTLEABPPHVLISR--PSAPFTASMMMSLTKLADKELVHMISWAKKI | 316 |
| Db | 306 | LALSITADQMVSALLDABFP--ILYSEYDPTREPFSEASMMGLTNLADRELVHMIMNAKRV | 364 |
| Qy | 317 | PGFVLSLFDQVRLLSCEWMEVLMGLMWRSIDHPKLI FAPDLVLDREBCKVEGILEI | 376 |
| Db | 365 | PGFVLTLDQVHLLCEAWLEILMIGLVWRSMEHPKLLFAPNLULDRNQKCVSGVVEI | 424 |
| Qy | 377 | FDMLLATSRFRELKLOHKEYLCVRAMILLNSSMYPLVTAT--QDADSSRKLAHLNNAVTD | 435 |
| Db | 425 | FDMLLATSRFRMNLQGBEFVCLAKIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKIID | 484 |
| Qy | 436 | ALVWVIAKSGISSQOSMELANLMLLSHVHASNKGMEHLNMMCKKNWVPYDLLLLLML | 495 |
| Db | 485 | TLIHLMAKAGLTQQOQHQLAQLLILSHIRMSNRKMEHLYSMCKKNWVPYDLLLLLML | 544 |
| Qy | 496 | NAHVL 500 | |
| Db | 545 | DAHRL 549 | |

Search completed: June 20, 2004, 10:44:38
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2004, 10:30:42 ; Search time 59 Seconds
(without alignments)
2538.139 Million cell updates/sec

Title: US-08-906-365-2
Perfect score: 2805
Sequence: 1 MDIKNSPSSLSNPSYNSQ.....ECSPAEDSKSEGSNQPSQ 530

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-----------|-------------|
| 1 | 2805 | 100.0 | 530 | AAW33215 | Human oes |
| 2 | 2805 | 100.0 | 530 | AAW37858 | Human oes |
| 3 | 2805 | 100.0 | 530 | AAW360649 | Human oes |
| 4 | 2805 | 100.0 | 530 | AAU27322 | Human oes |
| 5 | 2805 | 100.0 | 530 | AAE10457 | Human est |
| 6 | 2805 | 100.0 | 530 | AAE10457 | Human est |
| 7 | 2805 | 100.0 | 530 | ABG32754 | Nuclear r |
| 8 | 2805 | 100.0 | 530 | ADA83824 | Human BSR |
| 9 | 2805 | 100.0 | 530 | ABU61628 | Human oes |
| 10 | 2805 | 100.0 | 530 | ADE12138 | Human oes |
| 11 | 2805 | 100.0 | 548 | AAV07270 | Human oes |
| 12 | 2805 | 100.0 | 793 | ABE80756 | Amino aci |
| 13 | 2554 | 91.1 | 485 | AAW14724 | Human oes |
| 14 | 2535 | 90.4 | 485 | AAV01597 | An estrog |
| 15 | 2532 | 89.9 | 477 | AAW33212 | Human oes |
| 16 | 2522 | 89.9 | 477 | AAW47834 | Estrogen |
| 17 | 2502 | 89.2 | 549 | AAW98125 | Mouse oes |
| 18 | 2500 | 89.1 | 549 | AAV04434 | Murine mE |
| 19 | 2487.5 | 88.7 | 495 | ABJ72350 | Human oes |
| 20 | 2481 | 88.4 | 567 | AAW98128 | Mouse com |
| 21 | 2457 | 87.6 | 560 | AAV04433 | Murine mE |
| 22 | 2291 | 81.7 | 485 | AAW14723 | Rat oestr |
| 23 | 2291 | 81.7 | 485 | AAV01596 | An estrog |
| 24 | 2267 | 80.8 | 485 | AAW14725 | Mouse oes |
| 25 | 2245.5 | 80.1 | 510 | AAW98126 | Mouse oes |

| | | | | | | |
|----|--------|------|-----|---|----------|--------------------|
| 26 | 2245.5 | 80.1 | 510 | 2 | AAV04435 | AAV04435 Murine mE |
| 27 | 2231.5 | 79.6 | 474 | 3 | AAV51946 | AAV51946 Bovine ER |
| 28 | 2198 | 78.4 | 416 | 2 | AAW33213 | AAW33213 Human oes |
| 29 | 2198 | 78.4 | 416 | 5 | AAW47837 | AAW47837 ER splice |
| 30 | 2198 | 78.4 | 418 | 2 | AAW33214 | AAW33214 Human oes |
| 31 | 2198 | 78.4 | 418 | 5 | AAW47836 | AAW47836 ER splice |
| 32 | 1746 | 62.2 | 414 | 2 | AAW98127 | AAW98127 Rat oestr |
| 33 | 1746 | 62.2 | 730 | 2 | AAV04436 | AAV04436 Rat rER b |
| 34 | 1723 | 61.4 | 323 | 6 | ABJ72352 | ABJ72352 Human oes |
| 35 | 1636 | 58.3 | 320 | 5 | ABG32755 | ABG32755 Nuclear r |
| 36 | 1363 | 48.6 | 268 | 6 | ABU08038 | ABU08038 Human ste |
| 37 | 1235.5 | 44.0 | 581 | 5 | ABB83791 | ABB83791 Chemidoph |
| 38 | 1235.5 | 44.0 | 595 | 4 | AAW84509 | AAW84509 Human oes |
| 39 | 1233.5 | 44.0 | 595 | 2 | AAV21626 | AAV21626 Ligand bi |
| 40 | 1233.5 | 44.0 | 595 | 4 | AAW84505 | AAW84505 Human oes |
| 41 | 1233.5 | 44.0 | 595 | 4 | AAW84513 | AAW84513 Human oes |
| 42 | 1233.5 | 44.0 | 595 | 4 | AAW84506 | AAW84506 Human oes |
| 43 | 1233.5 | 44.0 | 595 | 5 | ABB76378 | ABB76378 Human nuc |
| 44 | 1231.5 | 43.9 | 595 | 4 | AAW84512 | AAW84512 Human oes |
| 45 | 1230.5 | 43.9 | 595 | 4 | AAW84507 | AAW84507 Human oes |

ALIGNMENTS

RESULT 1

AAW33215
ID AAW33215 standard; protein; 530 AA.

AC AAW33215;

XX 20-APR-1998 (first entry)

DE Human oestrogen receptor protein #2.

XX Oestrogen receptor protein; steroid; alternative splicing; estradiol;
KW estone; estriol; screening.

OS Homo sapiens.

XX EP798378-A2.

PN 01-OCT-1997.

XX 25-MAR-1997; 97EP-00200903.

XX 26-MAR-1996; 96EP-00200820.

XX 22-NOV-1996; 96EP-00203284.

XX (ALKU) AKZO NOBEL NV.

XX Mosselman S, Dijkema R;

XX WPI; 1997-473188/44.

XX N-PSDB; AAT88415.

XX DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues.

XX Claim 4; Page 35-37; 45pp; English.

XX This sequence represents a novel oestrogen binding protein isolated from human testis cDNA in order to study upstream translation-initiation codons using 5' RACE-PCR technology. This receptor is able to bind and be activated by estradiol, estone and estriol, can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues

XX Sequence 530 AA;

Query Match 100.0%; Score 2805; DB 2; Length 530;

Best Local Similarity 100.0%; Pred. No. 2.4e-258;

Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSYNSCSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60
 DB 1 MDIKNSPSSLSNPSYNSCSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60
 QY 61 NVTNLEGGPGRTTSPNVLPWPTPGHLSPLVVRQLSHLYAEQKSPWCEARSLEHTLPVN 120
 DB 61 NVTNLEGGPGRTTSPNVLPWPTPGHLSPLVVRQLSHLYAEQKSPWCEARSLEHTLPVN 120
 QY 121 RETLKRKVSNGRCASPTVTGSKRDHAFCAVCSYASGYHYGVMSCEGCKAFKRSIQGH 180
 DB 121 RETLKRKVSNGRCASPTVTGSKRDHAFCAVCSYASGYHYGVMSCEGCKAFKRSIQGH 180
 QY 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVKCSRRRCGYELVVRQRSADQLH 240
 DB 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVKCSRRRCGYELVVRQRSADQLH 240
 QY 241 CAGKAKSGGHPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPFTASMMSLTK 300
 DB 241 CAGKAKSGGHPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPFTASMMSLTK 300
 QY 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEMELANMLLSHVRHASKGMEHLINMK 360
 DB 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEMELANMLLSHVRHASKGMEHLINMK 360
 QY 361 VLDRDEGKCEGILEIFDMLLATTSRPRELKLQHKYELCVKAMILLNSSMYPVLTATQDA 420
 DB 361 VLDRDEGKCEGILEIFDMLLATTSRPRELKLQHKYELCVKAMILLNSSMYPVLTATQDA 420
 QY 421 DSSRKLHLNNAVTDALVWVIATKSGISSQQSQMELANMLLSHVRHASKGMEHLINMK 480
 DB 421 DSSRKLHLNNAVTDALVWVIATKSGISSQQSQMELANMLLSHVRHASKGMEHLINMK 480
 QY 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
 DB 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 2

AAW97858
 ID AAW97858 standard; protein; 530 AA.

NC AAW97858;

XX 07-JUN-1999 (first entry)

DE Human oestrogen receptor-beta.

XX Oestrogen receptor-beta; HER-beta; human.

XX Homo sapiens.

XX W09907847-A1.

XX 18-FEB-1999.

XX 20-JUL-1998; 98WO-US014944.

XX 05-AUG-1997; 97US-00906365.

XX (AMHP) AMERICAN HOME PROD CORP.

XX Bhat RA, Henderson RA, Hsiao C, Karathanasis SK;

XX WPI; 1999-167424/14.

XX N-PSDB; AAX24364.

XX Human oestrogen receptor-beta coding sequence - useful in the production
 of human oestrogen receptor-beta and identification of human oestrogen
 receptor-beta interactive compounds.

XX Claim 17; Page 42-44; 49pp; English.

XX

CC This polypeptide comprises a full-length human oestrogen receptor-beta
 (HER-beta), including 45 previously unknown N-terminal amino acid
 residues that are believed to contribute to the transcription activation
 function of the receptor. The amino acid sequence was deduced from the
 nucleotide sequence (see AAX24364) of an isolated cDNA clone. HER-beta is
 selectively expressed in the thymus, spleen, ovary and testes. The
 invention encompasses HER-beta polynucleotides and polypeptides,
 particularly peptides which include residues 1-45 of HER-beta. The
 invention also provides expression systems in which transcriptionally
 active HER-beta or fragments can be produced, as well as screening
 methods for identifying HER-beta agonists and antagonists (including
 tissue-specific oestrogens and anti-oestrogens), and HER-beta co-
 activators and inhibitors

XX Sequence 530 AA;

Query Match 100.0%; Score 2805; DB 2; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSYNSCSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60
 DB 1 MDIKNSPSSLSNPSYNSCSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60
 QY 61 NVTNLEGGPGRTTSPNVLPWPTPGHLSPLVVRQLSHLYAEQKSPWCEARSLEHTLPVN 120
 DB 61 NVTNLEGGPGRTTSPNVLPWPTPGHLSPLVVRQLSHLYAEQKSPWCEARSLEHTLPVN 120
 QY 121 RETLKRKVSNGRCASPTVTGSKRDHAFCAVCSYASGYHYGVMSCEGCKAFKRSIQGH 180
 DB 121 RETLKRKVSNGRCASPTVTGSKRDHAFCAVCSYASGYHYGVMSCEGCKAFKRSIQGH 180
 QY 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVKCSRRRCGYELVVRQRSADQLH 240
 DB 181 NDYICPATNQCTIDKNRRKSCQACRLKCYEVGMVKCSRRRCGYELVVRQRSADQLH 240
 QY 241 CAGKAKSGGHPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPFTASMMSLTK 300
 DB 241 CAGKAKSGGHPRVRELLDALSPEQLVLTLEAEPPHVLISRPSAPFTASMMSLTK 300
 QY 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEMELANMLLSHVRHASKGMEHLINMK 360
 DB 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCEMELANMLLSHVRHASKGMEHLINMK 360
 QY 361 VLDRDEGKCEGILEIFDMLLATTSRPRELKLQHKYELCVKAMILLNSSMYPVLTATQDA 420
 DB 361 VLDRDEGKCEGILEIFDMLLATTSRPRELKLQHKYELCVKAMILLNSSMYPVLTATQDA 420
 QY 421 DSSRKLHLNNAVTDALVWVIATKSGISSQQSQMELANMLLSHVRHASKGMEHLINMK 480
 DB 421 DSSRKLHLNNAVTDALVWVIATKSGISSQQSQMELANMLLSHVRHASKGMEHLINMK 480
 QY 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
 DB 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 3

AAW60649
 ID AAW60649 standard; protein; 530 AA.

XX AAW60649;

XX 04-MAY-2001 (first entry)

XX Human oestrogen receptor beta (ER-beta), SEQ ID NO:1.

XX Human oestrogen receptor beta; ER-beta; labelled hormone receptor;
 optical signal; ligand binding; hormonal disorder;
 sex hormone associated; ovulation; drug screening; drug discovery.

XX Homo sapiens.

XX

PN WC200107919-A1.
XX 01-FEB-2001.
XX 24-JUL-2000; 2000WO-JP004930.
XX 23-JUL-1999; 99JP-00209860.
PR 31-MAY-2000; 2000JP-00163475.
PR 31-MAY-2000; 2000JP-00163476.
XX (OLYU) OLYMPUS OPTICAL CO LTD.
PA Sakamoto H, Kato N;
XX WPI; 2001-168581/17.
XX N-PSDB; AAF59897.
XX Determination of the interaction of a substance for investigation and
PT diagnosis of hormonal disorders using an optically labelled receptor
PT protein.
XX Claim 26; Page 68-72; 75pp; Japanese.
XX The invention relates to a method for examining the interaction of a test
CC substance with a hormone receptor protein. The method involves contacting
CC a test substance with a hormone receptor protein (e.g., an oestrogen
CC receptor) which is labelled with an optical marker (e.g., a fluorescent
CC protein), where the marker is capable of undergoing a change in its
CC optical properties when the receptor binds a ligand. The optical signal
CC generated in the presence of the test compound is then compared with that
CC generated in the absence of the test compound to determine whether the
CC test compound is interacting with the hormone receptor protein. The
CC invention also encompasses the labelled hormone receptor protein, the
CC gene encoding it, and vectors and host cells comprising such genes. Of
CC method of the invention is used for the investigation and diagnosis of
CC hormonal disorders, especially those associated with sex hormones e.g.,
CC suppression of ovulation. The present sequence represents human oestrogen
CC receptor beta (ER-beta)
XX Sequence 530 AA;
SQ

Query Match 100.0%; Score 2805; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.4e-258; Mismatches 0; Indels 0; Gaps 0;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSINSPSSYNCSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60
DB 1 MDIKNSPSSINSPSSYNCSQILPLEHGSIIYIPSSYVDSHHEYPAMTFYSPAVMYSIPS 60
QY 61 NVTNLEGGGROTTSPNVLPPTPGHLSPLVVRQLSHLYABPKQSPWCBARSLHTLPVN 120
DB 61 NVTNLEGGGROTTSPNVLPPTPGHLSPLVVRQLSHLYABPKQSPWCBARSLHTLPVN 120
QY 121 RETLKRKVSNGRCASPVTPGSKRDAHFCAVCSVDVAGSYHYGVMSCEGCKAFPKRSIQH 180
DB 121 RETLKRKVSNGRCASPVTPGSKRDAHFCAVCSVDVAGSYHYGVMSCEGCKAFPKRSIQH 180
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DB 181 NDYICPATNQCTIDKNRKSQACRLKCYEYGVKQSGRRRCGRLVRRORSADQLH 240
QY 241 CAGKAKSGGAPRVREILLDALSPQVLITLLEAPPHVLSRSPAPTEASMMWSLTK 300
DB 241 CAGKAKSGGAPRVREILLDALSPQVLITLLEAPPHVLSRSPAPTEASMMWSLTK 300
QY 301 LADKELVEMISWAKIPGFVELSLFDQVALLSCWMEVLMGMLWRSIDHPGKLIAPDL 360
DB 301 LADKELVEMISWAKIPGFVELSLFDQVALLSCWMEVLMGMLWRSIDHPGKLIAPDL 360
QY 361 VLDRBGKCVGILETFDMLATTSPRELKLOHKEYLCVKAMILLNSMYPVLTATQDA 420
DB 361 VLDRBGKCVGILETFDMLATTSPRELKLOHKEYLCVKAMILLNSMYPVLTATQDA 420

QY 421 DSSRKLAEHLNAVTDALVWVIKSGISSQQSMRIANLMLLSHVHRHASNKGMEHLNNK 480
DB 421 DSSRKLAEHLNAVTDALVWVIKSGISSQQSMRIANLMLLSHVHRHASNKGMEHLNNK 480
QY 481 CKNVVPVYDLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSSONPQSQ 530
DB 481 CKNVVPVYDLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSSONPQSQ 530

RESULT 4
AAU27322
ID AAU27322 standard; protein; 530 AA.
XX AAU27322;
XX 18-DEC-2001 (first entry)
XX Human Oestrogen receptor beta.
XX Human; Oestrogen receptor beta; ERbeta; SNP; chromosome 6q.25.1;
KW single nucleotide polymorphism; cardiovascular disease;
KW autoimmune disease; systemic lupus erythematosus; arthritis; rheumatism;
KW osteoarthritis; osteoporosis; breast cancer; endometrial cancer.
XX Homo sapiens.
XX WO2000162793-A2.
XX 30-AUG-2001.
XX 20-FEB-2001; 2001WO-US005360.
XX 22-FEB-2000; 2000US-0183755P.
XX 24-JAN-2001; 2001US-00768185.
XX (PEKE) PE CORP NY.
XX Kalush F, Cassel MJ, Hwang SS, Winn-Deen ES;
XX WPI; 2001-582041/65.
XX N-PSDB; AAS43105, AAS43104.
XX Estrogen receptor gene and protein polymorphisms useful for diagnosis of
XX individuals at risk of developing bone disorders.
XX Disclosure; Fig 4; 245pp; English.
XX The invention relates to a novel isolated peptide comprising or
XX consisting of an amino acid sequence selected from an amino acid sequence
XX of a variant oestrogen receptor protein (e.g. ERbeta), or a fragment of
XX 10 amino acids), antibodies against them, nucleic acids encoding them
XX (including vectors for transforming cells). The gene for human ERbeta is
XX located on chromosome 6q.25.1. The variants are encoded by single
XX nucleotide polymorphisms (SNP). The variant peptides and proteins can be
XX used in assays to determine the biological activity of the protein, to
XX raise antibodies, as a reagent in assays designed to quantitatively
XX determine levels of the protein in biological fluids, to identify
XX compounds that modulate receptor activity and to screen compounds for the
XX ability to stimulate or inhibit interaction between the receptor protein
XX and a target molecule that normally interacts with the receptor protein
XX e.g. oestrogen. The antibody can be used to isolate the protein, to
XX assess expression in disease states e.g. cardiovascular disease and
XX autoimmune disease (e.g. systemic lupus erythematosus, arthritis,
XX rheumatism and osteoarthritis), osteoporosis, breast cancer and
XX endometrial cancer. In addition the antibodies can be used in
XX pharmacogenomic analysis and inhibiting protein function, e.g. blocking
XX the binding of the oestrogen receptor protein to a binding partner such
XX as a ligand. The nucleic acids encoding the proteins can be used as
XX probes, primers, chemical intermediates and in biological assays. The
XX present sequence represents human ERbeta
XX Sequence 530 AA;

Query Match 100.0%; Score 2805; DB 4; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNPSLSNPSYSCSILPLEHGSIIYPSYVDSHHEYPAMTFYSPAVNYSIPS 60
 DB 1 MDIKNPSLSNPSYSCSILPLEHGSIIYPSYVDSHHEYPAMTFYSPAVNYSIPS 60
 QY 61 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQSPWCCEARSLHTLPVN 120
 DB 61 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQSPWCCEARSLHTLPVN 120
 QY 121 RETLKRKVSNGRCASPVTPGSGKRDHAFCAVCSYASGYHYGVWSCGCKAPFKRSIQGH 180
 DB 121 RETLKRKVSNGRCASPVTPGSGKRDHAFCAVCSYASGYHYGVWSCGCKAPFKRSIQGH 180
 QY 181 NDYICPATNOCTIDKNRKSQACRLKCYEVMVKGSRRCRGYRLVRQRSADQLH 240
 DB 181 NDYICPATNOCTIDKNRKSQACRLKCYEVMVKGSRRCRGYRLVRQRSADQLH 240
 QY 241 CAGKARSGGHAPRVRELLDLSPEQLVLTLEAEPHVLISRPSPAPFTASMMSLTK 300
 DB 241 CAGKARSGGHAPRVRELLDLSPEQLVLTLEAEPHVLISRPSPAPFTASMMSLTK 300
 QY 301 LADKELVHMISWAKKIPGVFVLSLFDQVRLLESCEWELMGLMWSIDHPGKLIIFAPDL 360
 DB 301 LADKELVHMISWAKKIPGVFVLSLFDQVRLLESCEWELMGLMWSIDHPGKLIIFAPDL 360
 QY 361 VLDRDEGKCVGEILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPLVTATQDA 420
 DB 361 VLDRDEGKCVGEILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPLVTATQDA 420
 QY 421 DSSRKLHLNNAVTDALVWVIAKSGISSQQSWMELANMLLSHVHRASNKGMEHLNLMK 480
 DB 421 DSSRKLHLNNAVTDALVWVIAKSGISSQQSWMELANMLLSHVHRASNKGMEHLNLMK 480
 QY 481 CKNVVPVYDILLEMLNAHVLRCKSSITGSECSPAEDSKSKEGSONPQSQ 530
 DB 481 CKNVVPVYDILLEMLNAHVLRCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 5

AAB47835
 ID AAB47835 standard; protein; 530 AA.
 AC AAB47835;
 XX AAB47835;
 DT 18-DEC-2001 (first entry)
 DE Human estrogen receptor (ER)-beta protein.
 KW Estrogen receptor-beta; dietary compound; environmental pollutant;
 KW red wine; ER-beta mediated cell growth inhibition modulator; human.
 OS Homo sapiens.
 XX WO200169262-A1.
 XX 20-SEP-2001.
 XX 15-MAR-2001; 2001WO-US008276.
 XX 15-MAR-2000; 2000US-0189605P.
 XX (UYMA-) UNIV MASSACHUSETTS.
 PI Ho S;
 XX WPI; 2001-596920/67.
 DR N-PSDB; AAD18442.

In vitro screening for modulator of estrogen receptor-beta-mediated cell growth inhibition by contacting cell having functional ER-beta protein

PT with candidate compound and detecting ER-beta-regulated gene expression.
 XX Example 3; Fig 7A; 49pp; English.

CC The invention relates to in vitro screening for modulator of estrogen receptor-beta (ER-beta)-mediated cell growth inhibition. The method involves contacting mammalian cell having functional ER-beta protein with candidate compound and detecting increase/decrease of ER-beta-regulated gene expression in presence of candidate compound compared to expression in absence of the compound. The method is useful for identifying a compound that modulates ER-beta-mediated cell growth inhibition. It is useful for testing dietary compounds, e.g. red wine, for the presence of estrogen mimics that trigger ER-beta-mediated processes, thus affecting physiological function positively or negatively and for testing environmental pollutants for the presence of estrogen mimics that may pose health risks involving ER-beta-mediated processes. The present sequence is human ER-beta protein

SQ Sequence 530 AA;

Query Match 100.0%; Score 2805; DB 4; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNPSLSNPSYSCSILPLEHGSIIYPSYVDSHHEYPAMTFYSPAVNYSIPS 60
 DB 1 MDIKNPSLSNPSYSCSILPLEHGSIIYPSYVDSHHEYPAMTFYSPAVNYSIPS 60
 QY 61 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQSPWCCEARSLHTLPVN 120
 DB 61 NVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQSPWCCEARSLHTLPVN 120
 QY 121 RETLKRKVSNGRCASPVTPGSGKRDHAFCAVCSYASGYHYGVWSCGCKAPFKRSIQGH 180
 DB 121 RETLKRKVSNGRCASPVTPGSGKRDHAFCAVCSYASGYHYGVWSCGCKAPFKRSIQGH 180
 QY 181 NDYICPATNOCTIDKNRKSQACRLKCYEVMVKGSRRCRGYRLVRQRSADQLH 240
 DB 181 NDYICPATNOCTIDKNRKSQACRLKCYEVMVKGSRRCRGYRLVRQRSADQLH 240
 QY 241 CAGKARSGGHAPRVRELLDLSPEQLVLTLEAEPHVLISRPSPAPFTASMMSLTK 300
 DB 241 CAGKARSGGHAPRVRELLDLSPEQLVLTLEAEPHVLISRPSPAPFTASMMSLTK 300
 QY 301 LADKELVHMISWAKKIPGVFVLSLFDQVRLLESCEWELMGLMWSIDHPGKLIIFAPDL 360
 DB 301 LADKELVHMISWAKKIPGVFVLSLFDQVRLLESCEWELMGLMWSIDHPGKLIIFAPDL 360
 QY 361 VLDRDEGKCVGEILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPLVTATQDA 420
 DB 361 VLDRDEGKCVGEILEIFDMLLATTSRFRELKQHKYLCVKAMILLNSSMYPLVTATQDA 420
 QY 421 DSSRKLHLNNAVTDALVWVIAKSGISSQQSWMELANMLLSHVHRASNKGMEHLNLMK 480
 DB 421 DSSRKLHLNNAVTDALVWVIAKSGISSQQSWMELANMLLSHVHRASNKGMEHLNLMK 480
 QY 481 CKNVVPVYDILLEMLNAHVLRCKSSITGSECSPAEDSKSKEGSONPQSQ 530
 DB 481 CKNVVPVYDILLEMLNAHVLRCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 6

AAB47835
 ID AAB47835 standard; protein; 530 AA.
 AC AAB47835;
 XX AAB47835;
 DT 25-MAR-2002 (first entry)
 DE Full length estrogen receptor.

KW DNA binding domain; DBD; ligand binding domain; LBD; chimeric receptor;
 KW estrogen receptor; ER; chromosome 14; ER-alpha; ER-beta; exon 8;

KW estradiol; nuclear receptor; progesterone receptor.
 XX Homo sapiens.
 OS EP1162264-A2.
 PN DB 12-DEC-2001.
 PD 25-MAR-1997; 2001EP-00202021.
 PF 26-MAR-1996; 96EP-00200820.
 PR 22-NOV-1996; 96EP-00203284.
 PS 25-MAR-1997; 97EP-00200903.
 XX (ALKU) ARZO NOBEL NV.
 PA Mosselman S, Dijkema R;
 PI WPI; 2002-084414/12.
 DR N-PSDB; AAL72144.
 XX New isolated chimeric receptor comprising a DNA binding domain and/or
 PT ligand binding domain of a new estrogen receptor, for identifying
 PT functional ligands or hormonal analogs for the receptor.
 XX Example A; Page 26-28; 35pp; English.
 XX This sequence shows the full length novel estrogen receptor (ER). The
 CC additional N-terminal sequences of this sequence, compared to the ER
 CC sequence given in AAB47834, were generated using RACE PCR. The gene
 CC encoding this new ER is located on chromosome 14 and has a different
 CC tissue distribution from classical ER. This ER also has two orphan ER's,
 CC ER-alpha and ER-beta. These orphan receptors have estrogen receptor
 CC related structure but do not appear to be able to bind estradiol or other ER
 CC ligands. The DNA binding domain (DBD) and ligand binding domain (LBD)
 CC from this ER may be used in the chimeric receptor of the invention which
 CC also has an N-terminal domain. The chimeric receptor, or DNA encoding it,
 CC is useful in a screening assay for identification of new drugs. Similar
 CC chimeric receptors comprising the LBD of the new ER, and also comprising
 CC the DBD and an N-terminal domain derived from another nuclear receptor
 CC e.g., progesterone receptor, are useful for the screening of compounds to
 CC identify new ligands or hormone analogs which are able to activate the
 CC new ER. Chimeric receptors comprising a DBD of the new ER, and LBD and an
 CC N-terminal domain derived from another nuclear receptor, can be used to
 CC identify new ligands or hormone analogs for the nuclear receptors
 XX Sequence 530 AA;
 SQ

Query Match 100.0%; Score 2805; DB 5; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSLSNPSYNSQSILPLEHGSIVIPSSYVDSHHEYPANTFYSPAWNYSIPS 60
 DB 1 MDIKNSPSLSNPSYNSQSILPLEHGSIVIPSSYVDSHHEYPANTFYSPAWNYSIPS 60
 QY 61 NVTNLEGGPGQTTPSNVLPWTPPGHSLPLVVRQLSHLYABPQKSPWCARSLEHTLPWN 120
 DB 61 NVTNLEGGPGQTTPSNVLPWTPPGHSLPLVVRQLSHLYABPQKSPWCARSLEHTLPWN 120
 QY 121 RETLARKYGNRCASPVTPGSKRDHAFCAVCSDYASGVHYGVNSCECKAPFYKRSIQGH 180
 DB 121 RETLARKYGNRCASPVTPGSKRDHAFCAVCSDYASGVHYGVNSCECKAPFYKRSIQGH 180
 QY 181 NDYICPATNOCTIDNRRKSKOACRLKCYEYGVNKGSRERCGYRLVRQRSADEQLH 240
 DB 181 NDYICPATNOCTIDNRRKSKOACRLKCYEYGVNKGSRERCGYRLVRQRSADEQLH 240
 QY 241 CAGKAKSGGHAPRVRELLLDALSPEQLVLTLEAPPHVLIISPSAPFTFASMMMSLTK 300
 DB 241 CAGKAKSGGHAPRVRELLLDALSPEQLVLTLEAPPHVLIISPSAPFTFASMMMSLTK 300
 QY 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCHWMEVLMWGLMWSRIDHPGKLIIFAPDL 360

DB 301 LADKELVHMSWAKKIPGFVELSLFDQVRLLESCHWMEVLMWGLMWSRIDHPGKLIIFAPDL 360
 QY 361 VLDRDEKCKVEGILIEIFDMLLATTSRFRKLQHKSYLCVKAMILLNSSMYPLVATQDA 420
 DB 361 VLDRDEKCKVEGILIEIFDMLLATTSRFRKLQHKSYLCVKAMILLNSSMYPLVATQDA 420
 QY 421 DSSRKLAEHLNAVTDALVWVIAKSGISSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQ 530
 DB 421 DSSRKLAEHLNAVTDALVWVIAKSGISSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQ 530
 QY 481 CKNVVPPYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKGSGSONPQSQ 530
 DB 481 CKNVVPPYDILLLEMLNAHVLRGCKSSITGSECSPAEDSKSKGSGSONPQSQ 530

RESULT 7
 ABG32754
 ID ABG32754 standard; protein; 530 AA.
 XX AC ABG32754;
 XX 15-NOV-2002 (first entry)
 XX Nuclear receptor oestrogen beta (ER beta) protein.
 XX Human; nuclear receptor oestrogen beta; osteopathic; cytostatic;
 XX antiarteriosclerotic; neurotropic; neuroprotective; cardiant; cancer;
 XX osteoporosis; bone disease; reproductive disorder; atherosclerosis;
 XX cardiovascular disease; Alzheimer's disease.
 XX Homo sapiens.
 XX WO200264783-A2.
 XX 22-AUG-2002.
 XX 08-FEB-2002; 2002WO-EP001355.
 XX 09-FEB-2001; 2001EP-00103065.
 XX 16-MAY-2001; 2001EP-0011862.
 XX (LION-) LION BIOSCIENCE AG.
 XX Albers M, Ellwanger S, Loeser E, Koegl M;
 PI WPI; 2002-643484/69.
 DR N-PSDB; ABS53304.
 XX New nucleic acid molecule encoding cofactor (CF) 13, CF14 or CF15 of
 PT estrogen beta nuclear receptor for treating diseases, e.g. osteoporosis,
 PT cancer, atherosclerosis or Alzheimer's disease, screening assays and
 PT scientific research.
 XX Disclosure; Fig 4; 76pp; English.
 XX This invention relates to a novel isolated nucleic acid molecule coding
 CC for a cofactor of the oestrogen beta nuclear receptor. The proteins of
 CC the invention may have osteopathic, cytostatic, antiarteriosclerotic,
 CC neurotropic, neuroprotective and cardiant activity. The nucleic acid
 CC molecule is useful for encoding a cofactor of the oestrogen beta nuclear
 CC receptor which mediate estrogen receptor transactivation activity and
 CC thus, provide means for the treatment of numerous diseases such as
 CC osteoporosis and other bone diseases, failures in reproductive functions,
 CC cancer, cardiovascular diseases such as atherosclerosis as well as the
 CC prevention of hot flushes, mood changes and Alzheimer's disease. The
 CC cofactor proteins are also useful in screening for ligands of the
 CC oestrogen receptor beta, in screening drugs for agonist and antagonist
 CC activity, and as scientific research tools, e.g. for developing nucleic
 CC acid probes or anti-sense oligonucleotides. The proteins may also be used
 CC for developing antibodies for the detection of these proteins. Methods of
 CC the invention are useful for developing and identifying compounds for the
 CC treatment of the above diseases. The present sequence represents the

```

CC human oestrogen beta nuclear receptor protein (ER beta) of the invention
XX
SQ Sequence 530 AA;

Query Match      100.0%; Score 2805; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.4e-256;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSYNCSSQILPLEHGSIIYIPSSYVDSHHEYPAITFYSPAVMNSIPS 60
DB 1 MDIKNSPSSLSNPSYNCSSQILPLEHGSIIYIPSSYVDSHHEYPAITFYSPAVMNSIPS 60

QY 61 NVTNLEGGPGQRTTSPNVLWPTPGHLSPLVHRLSHLYAEPOKSPCEARSLEHTLPVN 120
DB 61 NVTNLEGGPGQRTTSPNVLWPTPGHLSPLVHRLSHLYAEPOKSPCEARSLEHTLPVN 120

QY 121 RETLKRKVSNGRCASPTVTPGSKEDAHFCAVCSDYASGYHYGWSCEGCKAFPKRSIQGH 180
DB 121 RETLKRKVSNGRCASPTVTPGSKEDAHFCAVCSDYASGYHYGWSCEGCKAFPKRSIQGH 180

QY 181 NDYICPATNQTIDKNRKSQACRLKCYEYGVKCGSRRCRGYRLVRRQRSADQLH 240
DB 181 NDYICPATNQTIDKNRKSQACRLKCYEYGVKCGSRRCRGYRLVRRQRSADQLH 240

QY 241 CAGKAKRSGGHAPRVRELLLDALSPQILVTLLEAPPHVLIISRPAPPTTEASMMSLTK 300
DB 241 CAGKAKRSGGHAPRVRELLLDALSPQILVTLLEAPPHVLIISRPAPPTTEASMMSLTK 300

QY 301 LADKELVHMI SWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWSRIDHPGKLI FAPDL 360
DB 301 LADKELVHMI SWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWSRIDHPGKLI FAPDL 360

QY 361 VLDRDEGKCVGILEIFDMLLATTSRPRELKHQKEYLCVKAMILLNSMYPVLTATQDA 420
DB 361 VLDRDEGKCVGILEIFDMLLATTSRPRELKHQKEYLCVKAMILLNSMYPVLTATQDA 420

QY 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQOSMRLANLLMLSHVHRHASKGMEHLNWK 480
DB 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQOSMRLANLLMLSHVHRHASKGMEHLNWK 480

QY 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
DB 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 8
ADA83824
ID ADA83824 standard; protein; 530 AA.
XX
XX ADA83824;
DT 20-NOV-2003 (first entry)
XX
XX Human ESR2 protein.
XX
XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;
XX stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
XX vaccine.
XX
XX Homo sapiens.
XX
XX W02002103028-A2.
XX
XX 27-DEC-2002.
XX
XX 30-MAY-2002; 2002MO-IB004189.
XX
XX 30-MAY-2001; 2001US-0293999P.
XX
XX 22-OCT-2001; 2001US-0330457P.
XX
XX 19-FEB-2002; 2002US-0357144P.
XX
XX (BIOM-) BIOMEDICAL CENT.
XX

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PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LI;
XX WPI: 2003-175241/17.
DR N-PSDB; ADA83823.
XX
XX Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX
XX Claim 29; Page 217-220; 516pp; English.
XX
XX The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence represents a
CC tumour-associated antigen of the invention.
XX
SQ Sequence 530 AA;

Query Match      100.0%; Score 2805; DB 6; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.4e-256;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSLSNPSYNCSSQILPLEHGSIIYIPSSYVDSHHEYPAITFYSPAVMNSIPS 60
DB 1 MDIKNSPSSLSNPSYNCSSQILPLEHGSIIYIPSSYVDSHHEYPAITFYSPAVMNSIPS 60

QY 61 NVTNLEGGPGQRTTSPNVLWPTPGHLSPLVHRLSHLYAEPOKSPCEARSLEHTLPVN 120
DB 61 NVTNLEGGPGQRTTSPNVLWPTPGHLSPLVHRLSHLYAEPOKSPCEARSLEHTLPVN 120

QY 121 RETLKRKVSNGRCASPTVTPGSKEDAHFCAVCSDYASGYHYGWSCEGCKAFPKRSIQGH 180
DB 121 RETLKRKVSNGRCASPTVTPGSKEDAHFCAVCSDYASGYHYGWSCEGCKAFPKRSIQGH 180

QY 181 NDYICPATNQTIDKNRKSQACRLKCYEYGVKCGSRRCRGYRLVRRQRSADQLH 240
DB 181 NDYICPATNQTIDKNRKSQACRLKCYEYGVKCGSRRCRGYRLVRRQRSADQLH 240

QY 241 CAGKAKRSGGHAPRVRELLLDALSPQILVTLLEAPPHVLIISRPAPPTTEASMMSLTK 300
DB 241 CAGKAKRSGGHAPRVRELLLDALSPQILVTLLEAPPHVLIISRPAPPTTEASMMSLTK 300

QY 301 LADKELVHMI SWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWSRIDHPGKLI FAPDL 360
DB 301 LADKELVHMI SWAKKIPGFVELSLFDQVRLLESCEWMEVLMGLMWSRIDHPGKLI FAPDL 360

QY 361 VLDRDEGKCVGILEIFDMLLATTSRPRELKHQKEYLCVKAMILLNSMYPVLTATQDA 420
DB 361 VLDRDEGKCVGILEIFDMLLATTSRPRELKHQKEYLCVKAMILLNSMYPVLTATQDA 420

QY 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQOSMRLANLLMLSHVHRHASKGMEHLNWK 480
DB 421 DSSRKLAHLNNAVTDALVWVIKSGISSQQOSMRLANLLMLSHVHRHASKGMEHLNWK 480

QY 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
DB 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

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RESULT 9
 ABU61628
 ID ABU61628 standard; protein; 530 AA.
 XX
 AC ABU61628;
 DT 11-AUG-2003 (first entry)
 XX
 DE Human oestrogen receptor beta, HERbeta.
 XX
 KW Human; oestrogen receptor beta; HER beta; receptor; FCS; FIDA;
 KW fluorescence correlation spectroscopy; green fluorescent protein; GFP;
 KW fluorescence intensity distribution analysis; nuclear receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2003022224-A1.
 XX
 PD 30-JAN-2003.
 XX
 PF 19-JUL-2002; 2002US-00198785.
 XX
 PR 19-JUL-2001; 2001JP-00220444.
 PR 23-JUL-2001; 2001JP-00221963.
 XX
 PA (OLYU) OLYMPUS OPTICAL CO LTD.
 XX
 PI Sakamoto H, Kato N, Okamoto N;
 XX
 DR WPI: 2003-479487/45.
 DR N-PSDB; AC61448.
 XX
 PT Detecting binding capacity of test substance, with respect to a protein,
 PT by reacting test substance with fluorescence-labeled protein and
 PT detecting change in the fluorescence intensity.
 XX
 PS Disclosure; Page 18-19; 30pp; English.
 XX
 CC The invention relates to detecting the presence/absence of binding
 CC capacity of a test substance, with respect to a protein, involves having
 CC a protein, which has been labeled with fluorescence material, exist in a
 CC solution and while successively measuring fluorescence intensity from the
 CC fluorescent material, reacting the test substance with labeled protein
 CC and determining binding capacity of the test substance, with respect to
 CC protein, on basis of successive change in fluorescent intensity. Also
 CC included is producing a protein which has been labeled with fluorescence,
 CC involving construction an expression vector by incorporating a gene
 CC encoding the protein, a gene encoding a fluorescent material for labeling
 CC the protein, and a promoter for expressing in vitro the gene encoding the
 CC protein, and having the expression vector exist in a solution which
 CC allows expression and transcription of the gene and production of the
 CC protein, thus producing the protein labeled with the fluorescent
 CC material. The protein is a hormone receptor (e.g. an oestrogen receptor),
 CC antigen or antibody. The method is useful for detecting a binding
 CC reaction of a test substance to a receptor, by maintaining a receptor
 CC (which has been labeled with a marker material capable of generating a
 CC light signal), a test substance, and a nucleic acid fragment having a
 CC specific nucleic acid sequence which allows binding of a receptor/ligand
 CC complex to it, in a solution in which the receptor and the ligand can
 CC form a complex and this receptor/ligand complex can be bound to the
 CC specific nucleic acid sequence, and detecting the presence/absence of the
 CC complex. The presence/absence of the receptor/test substance/nucleic acid
 CC fragment complex is detected by measuring diffusion time, in the
 CC solution, of the labeled receptor. The measurement is performed by
 CC fluorescence correlation spectroscopy (FCS) or fluorescence intensity
 CC distribution analysis (FIDA). The receptor is a nuclear receptor. The
 CC nucleic acid fragment having the specific nucleic acid sequence has
 CC molecular weight which is not smaller than that of the receptor, and a
 CC diffusion constant which is not larger than that of the receptor. Binding
 CC affinity of the test substance with respect to the receptor is evaluated
 CC by expressing, through calculation using an autocorrelation function, the

CC amount of the receptor monomer and the amount of the receptor/test
 CC substance/nucleic acid fragment complex with relative values. The nucleic
 CC acid is DNA. The detection is carried out according to high-throughput
 CC detection. The present sequence represents human oestrogen receptor beta
 CC (HERbeta) which is coupled to green fluorescent protein (GFP) and used in
 CC the method of the invention
 XX

SQ Sequence 530 AA;

Query Match 100.0%; Score 2805; DB 7; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.4e-258;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MDIKNSPSSLSNPSYNCSSILPLEHGSYIIPSSYVDSHHHEYPAMFYSPAVNYSIPS 60
 Db 1 MDIKNSPSSLSNPSYNCSSILPLEHGSYIIPSSYVDSHHHEYPAMFYSPAVNYSIPS 60
 Qy 61 NVTNLEGGPGRTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQKSPWCEAFSLHTLPVN 120
 Db 61 NVTNLEGGPGRTTSPNVLWPTPGHLSPLVVRQLSHLYAEPQKSPWCEAFSLHTLPVN 120
 Qy 121 RETLKRKVSNGRCASPVTPGSGKDDAHPCAVCSYASGYHYGWSCEGCKAFFKRSIQGH 180
 Db 121 RETLKRKVSNGRCASPVTPGSGKDDAHPCAVCSYASGYHYGWSCEGCKAFFKRSIQGH 180
 Qy 181 NDYICPATNCTIDKNRKKSCQACRLKCYEVGVKCGSRRCRGYRLVRRQSADEQLH 240
 Db 181 NDYICPATNCTIDKNRKKSCQACRLKCYEVGVKCGSRRCRGYRLVRRQSADEQLH 240
 Qy 241 CAGKAKSGGHAHPVRRELLLDALSPQLVLTLEAPRPHVLISRPSPAPFTTASMMMSLTK 300
 Db 241 CAGKAKSGGHAHPVRRELLLDALSPQLVLTLEAPRPHVLISRPSPAPFTTASMMMSLTK 300
 Qy 301 LADKELVHMLSWAKKIGFVVELSLFDQVRLLESCEMVEMLMGLMWRSIDHPGKLIIFAPDL 360
 Db 301 LADKELVHMLSWAKKIGFVVELSLFDQVRLLESCEMVEMLMGLMWRSIDHPGKLIIFAPDL 360
 Qy 361 VLDRECKCVEGILEIFDMLLATTSTRRELKQHKBYLCVKAMILLNSSMPLVTATODA 420
 Db 361 VLDRECKCVEGILEIFDMLLATTSTRRELKQHKBYLCVKAMILLNSSMPLVTATODA 420
 Qy 421 DSSKRLAHLLNAVTDALVWVIKSGISSQOOSMELANILLSHVHRASNKGMEHLLNMK 480
 Db 421 DSSKRLAHLLNAVTDALVWVIKSGISSQOOSMELANILLSHVHRASNKGMEHLLNMK 480
 Qy 481 CKNVVPYDILLENLNAHVLRGCKSSITGSECSPAEDSKSGEQSNPQSQ 530
 Db 481 CKNVVPYDILLENLNAHVLRGCKSSITGSECSPAEDSKSGEQSNPQSQ 530

RESULT 10

ADE12138
 ID ADE12138 standard; protein; 530 AA.

XX ADE12138;

XX 29-JAN-2004 (first entry)

DE Human oestrogen receptor beta.

KW Human; oestrogen receptor beta;

KW oestrogen-dependent genitourinary condition; leiomyoma; fibroid;
 KW pregnancy prevention; gynaecological; cytostatic; contraceptive;
 KW receptor.

OS Homo sapiens.

XX US2003199472-A1.

XX 23-OCT-2003.

XX 19-MAR-2003; 2003US-00192274.

XX


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PR 19-MAR-2002; 2002US-0365760P.
XX (TEXA ) UNIV TEXAS SYSTEM.
PA (NOUN ) UNIV NORTHWESTERN.
XX
XX AJ-Hendy A, Lee EJ, Jameson JL;
XX PI
XX WPI; 2003-852811/79.
DR N-PSDB; ADE12137.
XX
XX Treating an estrogen-dependent genitourinary condition in a patient by
PT administering to the patient an expression construct comprising a nucleic
PT acid sequence encoding a modified estrogen receptor e.g., leiomyoma or
PT fibroid.
XX
XX Claim 27; SEQ ID NO 4; 45pp; English.
XX
XX The invention relates to a method for treating an oestrogen-dependent
CC genitourinary condition in a patient comprising administering an
CC expression construct comprising a nucleic acid sequence encoding a
CC modified oestrogen receptor. The sequence is under the control of a
CC promoter. The method is useful for treating an oestrogen-dependent
CC genitourinary condition in a patient, e.g., leiomyoma or fibroids, or for
CC preventing pregnancy. This sequence represents the human oestrogen
CC receptor beta polypeptide of the invention.
XX
XX Sequence 530 AA;
XX
Query Match 100.0%; Score 2805; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.4e-258;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSSHHEYPAMTFYSPAVMYSIPS 60
DB 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSSHHEYPAMTFYSPAVMYSIPS 60
QY 61 NVTNLEGGGRQTTSPNVLTPTGHLSPVVRHQLSHLYABPQKSPWCARSLEHTLPVN 120
DB 61 NVTNLEGGGRQTTSPNVLTPTGHLSPVVRHQLSHLYABPQKSPWCARSLEHTLPVN 120
QY 121 RETLKRKVSNGRCASPTVPGSKRDAHFCVCSYASGYHYGWSCEGCKAFPKRSIQGH 180
DB 121 RETLKRKVSNGRCASPTVPGSKRDAHFCVCSYASGYHYGWSCEGCKAFPKRSIQGH 180
QY 181 NDYICPATNQCTIDKNRKSQACRLRKCYEVMVKCGSRRCGRLVVRQRSADQLH 240
DB 181 NDYICPATNQCTIDKNRKSQACRLRKCYEVMVKCGSRRCGRLVVRQRSADQLH 240
QY 241 CAGKAKRSGGHAPRVRELLLDALSPQLVTLLEAPPHVLSRPSAPPTASMMSLTK 300
DB 241 CAGKAKRSGGHAPRVRELLLDALSPQLVTLLEAPPHVLSRPSAPPTASMMSLTK 300
QY 301 LADKELVHMIISWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLIAPDL 360
DB 301 LADKELVHMIISWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLIAPDL 360
QY 361 VLDRDGKCVGELIETFDMLATTSRFRKLQHKYLCVKAMILLNSSMYPLVATQDA 420
DB 361 VLDRDGKCVGELIETFDMLATTSRFRKLQHKYLCVKAMILLNSSMYPLVATQDA 420
QY 421 DSSRKLHLNLAVTDALVWYIAKSGISSQQSMRLANLLMLLSVHRASNKGMHLLNMK 480
DB 421 DSSRKLHLNLAVTDALVWYIAKSGISSQQSMRLANLLMLLSVHRASNKGMHLLNMK 480
QY 481 CKNVWPVYDLEMLNAHVLGRCKSSITGSECSPAEDSKSKEGSONPQSQ 530
DB 481 CKNVWPVYDLEMLNAHVLGRCKSSITGSECSPAEDSKSKEGSONPQSQ 530

```

RESULT 11

AAY07270

ID AAY07270 standard; protein: 548 AA.

XX

```

AC AAY07270;
XX 06-JUL-1999 (first entry)
XX Human oestrogen receptor.
XX
XX Human; oestrogen receptor; ligand; bone resorption; metabolic disorder;
XX cardiovascular disease; cancer; central nervous system; breast; uterine;
XX osteoporosis; ovarian; prostate; diabetes; Alzheimer's disease.
XX
XX Homo sapiens.
XX WO9912961-A1.
XX 18-MAR-1999.
XX
XX 04-SEP-1998; 98WO-US018577.
XX
XX 08-SEP-1997; 97US-0058271P.
XX 30-SEP-1997; 97US-0060520P.
XX 30-OCT-1997; 97GB-00022884.
XX 20-MAR-1998; 98GB-00006032.
XX (MERI ) MERCK & CO INC.
XX Wilkinson H;
XX WPI; 1999-229222/19.
XX N-PSDB; AAX34309.
XX
XX Estrogen receptor useful in ligand identification in medicine.
XX
XX Claim 1; Fig 1; 32pp; English.
XX
XX This sequence represents a human oestrogen receptor. The receptor can be
XX used to identify ligands that bind to human oestrogen receptor. The
XX ligands can be used in a method for preventing or treating an oestrogen
XX receptor mediated disease or condition, such as abnormal bone resorption,
XX a cardiovascular disease, cancer, metabolic disorders, or central nervous
XX system disorders. The ligand is especially used to treat osteoporosis,
XX breast, uterine, ovarian or prostate cancer, diabetes or Alzheimer's
XX disease
XX
XX Sequence 548 AA;
XX
Query Match 100.0%; Score 2805; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.5e-258;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSSHHEYPAMTFYSPAVMYSIPS 60
DB 19 MDIKNSPSSLSNPSYNSQSILPLEHGSIIYIPSSYVDSSHHEYPAMTFYSPAVMYSIPS 78
QY 61 NVTNLEGGGRQTTSPNVLTPTGHLSPVVRHQLSHLYABPQKSPWCARSLEHTLPVN 120
DB 79 NVTNLEGGGRQTTSPNVLTPTGHLSPVVRHQLSHLYABPQKSPWCARSLEHTLPVN 138
QY 121 RETLKRKVSNGRCASPTVPGSKRDAHFCVCSYASGYHYGWSCEGCKAFPKRSIQGH 180
DB 139 RETLKRKVSNGRCASPTVPGSKRDAHFCVCSYASGYHYGWSCEGCKAFPKRSIQGH 198
QY 181 NDYICPATNQCTIDKNRKSQACRLRKCYEVMVKCGSRRCGRLVVRQRSADQLH 240
DB 199 NDYICPATNQCTIDKNRKSQACRLRKCYEVMVKCGSRRCGRLVVRQRSADQLH 258
QY 241 CAGKAKRSGGHAPRVRELLLDALSPQLVTLLEAPPHVLSRPSAPPTASMMSLTK 300
DB 259 CAGKAKRSGGHAPRVRELLLDALSPQLVTLLEAPPHVLSRPSAPPTASMMSLTK 318
QY 301 LADKELVHMIISWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLIAPDL 360
DB 319 LADKELVHMIISWAKKIPGFVELSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLIAPDL 378

```

QY 361 VLDRBCKVEGILEIFDMLLATTSRFRELKLOHKEYLCKVAMILLNSSMYPLVTATQDA 420
 DB 379 VLDRBCKVEGILEIFDMLLATTSRFRELKLOHKEYLCKVAMILLNSSMYPLVTATQDA 438
 QY 421 DSSRKLHLNAVTDALVWVIAKSGISSQQSMELANLMLLSHVRHASKNGHEHLNWK 480
 DB 439 DSSRKLHLNAVTDALVWVIAKSGISSQQSMELANLMLLSHVRHASKNGHEHLNWK 498
 QY 481 CKNVVPYDILLEMLNAFVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
 DB 499 CKNVVPYDILLEMLNAFVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 548

RESULT 12

ABB80756
 ID ABB80756 standard; protein; 793 AA.

XX AC ABB80756;

XX DT 23-SEP-2002 (first entry)

XX DE Amino acid sequence of a fusion GFP/HER beta protein.

XX KW Fluorometric analyzer; laser; fluorescence; GFP; ER beta; human; gene;
 XX KW green fluorescent protein; estrogen receptor beta; fusion protein.

XX OS Synthetic.

XX OS Aequorea victoria.

XX OS Homo sapiens.

XX PN W0200248693-A1.

XX PX 20-JUN-2002.

XX PF 14-DEC-2001; 2001WO-JP010998.

XX PR 14-DEC-2000; 2000JP-00380327.

XX PR 30-JAN-2001; 2001JP-00022105.

XX PA (OLYU) OLYMPUS OPTICAL CO LTD.

XX PI Kato N, Sakamoto H;

XX DR WPI; 2002-528176/56.

XX DR N-PSDB; ABN86125.

XX PT Autocorrection function-embedded confocal optics-based fluorometric
 XX PT analyzers for studying behaviors of fluorescence-labeled molecules
 XX PT particularly intracellular biological molecules like proteins at
 XX PT molecular level.

XX PS Example 2; Page 98-105; 109pp; Japanese.

XX CC The invention relates to a fluorometric analyzer that comprises a laser
 CC light source, an optical system for focusing the light beam from laser
 CC light source to a sample to form a confocal region, another optical
 CC system for focusing fluorescence from the sample, a light detector for
 CC measuring intensity, and a recording means to record the variation of
 CC intensity in the measured fluorescence. The analyzers are for studying
 CC behaviors of fluorescence-labeled molecules particularly intracellular
 CC biological molecules like proteins at molecular level, e.g. protein
 CC functions and interactions. Such analyzers are stable and convenient to
 CC operate, thereby enabling easy performance of fluorescence correlation
 CC spectroscopy, fluorescence intensity distribution analysis and
 CC fluorescence intensity multiple distribution analysis. The present
 CC sequence represents the amino acid sequence of a fusion protein
 CC comprising a GFP (green fluorescent protein) and HER (human estrogen
 CC receptor) beta protein

XX SQ Sequence 793 AA;

Query Match 100.0%; Score 2805; DB 5; Length 793;

Best Local Similarity 100.0%; Pred. No. 4.4e-258;

| | Matches | 530; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|----|---------|--------------|--------------|---------------------|-----------------------|--------------|-------------|-------------|------------|-----------------|
| QY | 1 | MDIKNSPSSINS | PSSNCSQ | SILPLEHGSIIYIPSSVDS | SHHEYPAMTFYSPAMNTSIPS | 60 | | | | |
| DB | 264 | MDIKNSPSSINS | PSSNCSQ | SILPLEHGSIIYIPSSVDS | SHHEYPAMTFYSPAMNTSIPS | 323 | | | | |
| QY | 61 | NVTNLGGG | PGROTTSPNV | LPWPTPGHLSPLV | VRHQLSHLYAEPKSPWC | EARSLHETLPVN | 120 | | | |
| DB | 324 | NVTNLGGG | PGROTTSPNV | LPWPTPGHLSPLV | VRHQLSHLYAEPKSPWC | EARSLHETLPVN | 383 | | | |
| QY | 121 | RETLK | KEKVS | GNRCAS | PVTGPGSKRDAH | FCACVCS | DYASGVHYG | WVMSCEGCKAF | FKRSIQGH | 443 |
| DB | 384 | RETLK | KEKVS | GNRCAS | PVTGPGSKRDAH | FCACVCS | DYASGVHYG | WVMSCEGCKAF | FKRSIQGH | 443 |
| QY | 181 | NDYIC | PATNQCTID | KNRKSCQ | ACRLRKCYE | GVGK | WVMSCEGCKAF | FKRSIQGH | 443 | |
| DB | 444 | NDYIC | PATNQCTID | KNRKSCQ | ACRLRKCYE | GVGK | WVMSCEGCKAF | FKRSIQGH | 443 | |
| QY | 241 | CAGKAK | SGGHAP | RVRELL | LDALSP | QQLVLT | LEAEP | PHVLI | SRPSAP | FT |
| DB | 504 | CAGKAK | SGGHAP | RVRELL | LDALSP | QQLVLT | LEAEP | PHVLI | SRPSAP | FT |
| QY | 301 | LADKEL | VHMTIS | NAKKIP | GFVLSL | PDQVRL | BSCW | MEVLM | GMGLM | RSIDHPGKL |
| DB | 564 | LADKEL | VHMTIS | NAKKIP | GFVLSL | PDQVRL | BSCW | MEVLM | GMGLM | RSIDHPGKL |
| QY | 361 | VLDR | BCKVEG | ILEIFD | MLLATT | SRFREL | KLOH | KEYL | CKV | KAMI |
| DB | 624 | VLDR | BCKVEG | ILEIFD | MLLATT | SRFREL | KLOH | KEYL | CKV | KAMI |
| QY | 421 | DSSR | KLHLNAV | TDALV | WVIAK | SGISS | QQSM | ELANL | MLLSH | VRHASKNGHEHLNWK |
| DB | 684 | DSSR | KLHLNAV | TDALV | WVIAK | SGISS | QQSM | ELANL | MLLSH | VRHASKNGHEHLNWK |
| QY | 481 | CKNV | VPYDILLE | MLNAF | VLRG | CKSSIT | GSECS | PAEDSKS | KEGSONPQSQ | 530 |
| DB | 744 | CKNV | VPYDILLE | MLNAF | VLRG | CKSSIT | GSECS | PAEDSKS | KEGSONPQSQ | 793 |

RESULT 13

AAW14724

ID AAW14724 standard; protein; 485 AA.

XX AC AAW14724;

XX DT 08-JUN-1997 (first entry)

XX DE Human oestrogen receptor beta (ER-beta).

XX KW Orphan receptor; oestrogen receptor beta; ER-beta; nuclear receptor;
 XX KW prostate cancer; benign prostatic hyperplasia; ovary cancer;
 XX KW cardiovascular disease; osteoporosis; environment; pollutant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 104..169

XX FT Domain /label=DNA-binding_domain

XX FT Domain 260..457

XX FT Domain /label=Ligand-binding_domain

XX PN W09709348-A2.

XX PD 13-MAR-1997.

XX PX 09-SEP-1996; 96WO-EP003933.

XX PR 08-SEP-1995; 95GE-00018272.

XX PR 15-MAR-1996; 96GE-00005550.

XX PR 11-APR-1996; 96GE-00007532.

XX PR 08-MAY-1996; 96GE-00009576.

XX PA (KARO-) KARO BIO AB.

XX PI Kuiper GG, Bumark E, Gustafsson J;
XX KW WPI: 1997-192842/17.
XX DR N-PSDB; AAT62843.
XX PT New isolated oestrogen receptor beta - used to develop prods. for
XX PT treating e.g. cancers, CNS diseases, osteoporosis or cardiovascular
XX PT disease.
XX PS Claim 1; Fig 13A; 45pp; English.
XX CC A novel human orphan receptor (AAW14724) is related to the known
XX CC oestrogen receptor ER-alpha, and has been designated ER-beta. It is an
XX CC oestrogen receptor-related nuclear receptor. The ER-beta amino acid
XX CC sequence was deduced from a cDNA clone (AAT62843) isolated from a human
XX CC testis cDNA library. Rat, human and mouse ER-beta (AAW14723-25) can be
XX CC used to isolate molecules for use in the treatment of cardiovascular
XX CC diseases, central nervous system diseases, osteoporosis, prostate or
XX CC ovarian cancer or benign prostatic hyperplasia and to test environmental
XX CC chemicals for oestrogenic activity
XX CC
SQ Sequence 485 AA;
Query Match 91.1%; Score 2554; DB 2; Length 485;
Best Local Similarity 99.8%; Pred. No. 1.9e-234; Mismatches 1; Indels 0; Gaps 0;
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 46 MTFYSPAVMYNIPSNVTNLEGGPGQRTTSPNVLMPPTGHLSPVLVHRLSHLYAEPOKS 105
Db 1 MTFYSPAVMYNIPSNVTNLEGGPGQRTTSPNVLMPPTGHLSPVLVHRLSHLYAEPOKS 60
QY 106 PWCEARSLHTLPVNRRLTKRKVSGNRCASPTVGSKSDAHFCAVCSYASGYHYGWS 165
Db 61 PWCEARSLHTLPVNRRLTKRKVSGNRCASPTVGSKSDAHFCAVCSYASGYHYGWS 120
QY 166 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRRKSCQACLRKCYEYGVWVKGSRRCG 225
Db 121 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRRKSCQACLRKCYEYGVWVKGSRRCG 180
QY 226 YRLVRRQRSADQLHCAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPPHVLISRP 285
Db 181 YRLVRRQRSADQLHCAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPPHVLISRP 240
QY 286 SAPFTASMMSLTKLADKELVHMI SWAKKIPGVVELSLFDQVRLLESQWMEVLMGLMW 345
Db 241 SAPFTASMMSLTKLADKELVHMI SWAKKIPGVVELSLFDQVRLLESQWMEVLMGLMW 300
QY 346 RSIDHPGKLI FAPDLVLRDRDEGKCVGILEIFDMLLATTSSRPRELKLQHKVLCVKAMIL 405
Db 301 RSIDHPGKLI FAPDLVLRDRDEGKCVGILEIFDMLLATTSSRPRELKLQHKVLCVKAMIL 360
QY 406 LNSSMYPLVTATODADSSRLAHLNAVTDALVWIAKSGISSQQSQSMELANLLMLLSHV 465
Db 361 LNSSMYPLVTATODADSSRLAHLNAVTDALVWIAKSGISSQQSQSMELANLLMLLSHV 420
QY 466 RHASNKGMEHLLNMCKNNVVPVYDILLEMLNAHVLRGCKSSITGSCSPAESKSKGEGSQ 525
Db 421 RHASNKGMEHLLNMCKNNVVPVYDILLEMLNAHVLRGCKSSITGSCSPAESKSKGEGSQ 480
QY 526 NPQSQ 530
Db 481 NPQSQ 485
RESULT 14
ID AAY01597
XX AAY01597 standard; protein; 485 AA.
AC AAY01597;
XX AAY01597;
DT 17-JUN-1999 (first entry)
XX

DE An estrogen receptor-beta protein.
XX differential estrogen receptor; ER-alpha; ER-beta; activation; API site;
XX therapy.
XX Homo sapiens.
XX OS
XX W09911760-A1.
XX EN
XX 11-MAR-1999.
XX PD
XX 31-AUG-1998; 98WO-US018030.
XX PF
XX 04-SEP-1997; 97US-00923708.
XX PR
XX (REGC) UNIV CALIFORNIA.
XX EA
XX Kushner FJ, Gustafsson J, Kuiper GGJM, Nilsson S, Paech K;
XX PI Scanlan TS, Webb P;
XX PI
XX WPI: 1999-205173/17.
XX DR N-PSDB; AAX26686.
XX PT
XX Screening for test compounds which inhibit or activate estrogen receptor
XX beta (ER-beta) mediated activation at a API site - for use in therapy.
XX PS Claim 14; Page 43-44; 61pp; English.
XX CC The present sequence represents an estrogen receptor-beta. The
XX CC specification describes a method for screening test compounds for
XX CC differential estrogen receptor (ER) alpha-mediated and ER beta-mediated
XX CC activation at an API site. The method is used for identifying compounds
XX CC which can be used in therapy
XX CC
SQ Sequence 485 AA;
Query Match 90.4%; Score 2535; DB 2; Length 485;
Best Local Similarity 99.2%; Pred. No. 1.2e-232; Mismatches 4; Indels 0; Gaps 0;
Matches 481; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 46 MTFYSPAVMYNIPSNVTNLEGGPGQRTTSPNVLMPPTGHLSPVLVHRLSHLYAEPOKS 105
Db 1 MTFYSPAVMYNIPSNVTNLEGGPGQRTTSPNVLMPPTGHLSPVLVHRLSHLYAEPOKS 60
QY 106 PWCEARSLHTLPVNRRLTKRKVSGNRCASPTVGSKSDAHFCAVCSYASGYHYGWS 165
Db 61 PWCEARSLHTLPVNRRLTKRKVSGNRCASPTVGSKSDAHFCAVCSYASGYHYGWS 120
QY 166 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRRKSCQACLRKCYEYGVWVKGSRRCG 225
Db 121 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRRKSCQACLRKCYEYGVWVKGSRRCG 180
QY 226 YRLVRRQRSADQLHCAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPPHVLISRP 285
Db 181 YRLVRRQRSADQLHCAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPPHVLISRP 240
QY 286 SAPFTASMMSLTKLADKELVHMI SWAKKIPGVVELSLFDQVRLLESQWMEVLMGLMW 345
Db 241 SAPFTASMMSLTKLADKELVHMI SWAKKIPGVVELSLFDQVRLLESQWMEVLMGLMW 300
QY 346 RSIDHPGKLI FAPDLVLRDRDEGKCVGILEIFDMLLATTSSRPRELKLQHKVLCVKAMIL 405
Db 301 RSIDHPGKLI FAPDLVLRDRDEGKCVGILEIFDMLLATTSSRPRELKLQHKVLCVKAMIL 360
QY 406 LNSSMYPLVTATODADSSRLAHLNAVTDALVWIAKSGISSQQSQSMELANLLMLLSHV 465
Db 361 LNSSMYPLVTATODADSSRLAHLNAVTDALVWIAKSGISSQQSQSMELANLLMLLSHV 420
QY 466 RHASNKGMEHLLNMCKNNVVPVYDILLEMLNAHVLRGCKSSITGSCSPAESKSKGEGSQ 525
Db 421 RHASNKGMEHLLNMCKNNVVPVYDILLEMLNAHVLRGCKSSITGSCSPAESKSKGEGSQ 480
QY 526 NPQSQ 530

QY 354 LIFAPDLVDRDEGKCVGILEIFDMLLATTSRRELKLOHKEYLCVKAMILLNSSMYPL 413
DB 301 LIFAPDLVDRDEGKCVGILEIFDMLLATTSRRELKLOHKEYLCVKAMILLNSSMYPL 360
QY 414 VTATODADSSRKLALHNAVTDALVWVIKSGISSQSSMRLANLMLLSHVHSHKGM 473
DB 361 VTATODADSSRKLALHNAVTDALVWVIKSGISSQSSMRLANLMLLSHVHSHKGM 420
QY 474 EHLNKKCNVVPVVDLLEMLNAHVLRGCKSSITSECSPAEDSKSKGSONPQSQ 530
DB 421 EHLNKKCNVVPVVDLLEMLNAHVLRGCKSSITSECSPAEDSKSKGSONPQSQ 477

Search completed: June 20, 2004, 10:37:11
Job time : 62 secs

DB 481 NLQSQ 485
RESULT 15
ID AAW33212 standard; protein; 477 AA.
AAW33212;
20-APR-1998 (first entry)
DE Human oestrogen receptor protein.
KW Oestrogen receptor protein; steroid; alternative splicing; estradiol;
KW estone; estrinol; screening.
OS Homo sapiens.
PN EP798378-A2.
XX PD 01-OCT-1997.
XX PF 25-MAR-1997; 97EP-00200903.
XX PR 26-MAR-1996; 96EP-00200820.
XX PR 22-NOV-1996; 96EP-00203284.
XX PA (ALKU) AKZO NOBEL NV.
XX PI Mosselman S, Dijkema R;
XX WPI; 1997-473188/44.
XX DR N-PSDB; AAT88412.
XX PT DNA encoding estrogen receptor - useful in screening assay to identify
XX novel ligands or hormonal analogues.
XX PS Claim 4; Page 18-20; 45pp; English.
XX CC This sequence represents a novel oestrogen binding protein. The cDNA
XX sequence which encodes this protein can be alternatively spliced
XX resulting in the detection of additional transcripts (see AAT88413). This
XX receptor is able to bind and be activated by estradiol, estone and
XX estrinol, can be used in a screening assay for the identification of new
XX drugs e.g. novel ligands or hormonal analogues
SQ Sequence 477 AA;
Query Match 89.9%; Score 2522; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.1e-231; Indels 0; Gaps 0;
Matches 477; Conservative 0; Mismatches 0;
QY 54 MNYISPSNVTLGGPGRQTTPNVLWPTPGHLSPLVVRQLSHLYAEPQKSPWCEARSL 113
DB 1 MNYISPSNVTLGGPGRQTTPNVLWPTPGHLSPLVVRQLSHLYAEPQKSPWCEARSL 60
QY 114 EHTLPVNRETLKRKVSNGRCASPTVGRSKEDAHFCAVCSDYASGYHYGWSCEGCKAPP 173
DB 61 EHTLPVNRETLKRKVSNGRCASPTVGRSKEDAHFCAVCSDYASGYHYGWSCEGCKAPP 120
QY 174 KRISQGHNDYICPATNCTIDKNRKSQAQRLKCYEYGVKCGSRRCGYRLVRQR 233
DB 121 KRISQGHNDYICPATNCTIDKNRKSQAQRLKCYEYGVKCGSRRCGYRLVRQR 180
QY 234 SADEQLHCAGKAKSGGHAPVRILLDLSPQOLVLTLEAPPVHLISRPSAPFEAS 293
DB 181 SADEQLHCAGKAKSGGHAPVRILLDLSPQOLVLTLEAPPVHLISRPSAPFEAS 240
QY 294 MMSLTKLADKELVHMISWAKKIFGVFVLSLFDQVRLLESQWMEVLMWGLMWSIDHPGX 353
DB 241 MMSLTKLADKELVHMISWAKKIFGVFVLSLFDQVRLLESQWMEVLMWGLMWSIDHPGX 300

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OM protein - protein search, using sw model
Run on: June 20, 2004, 10:35:07 ; Search time 21 seconds
(without alignments)
2427.691 Million cell updates/sec

Title: US-08-906-365-2
Perfect score: 2805
Sequence: 1 MDIKNSPSSNSPSSVNCQ.....ECSPAEDSKSKEGQNPOSQ 530
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seg length: 0
Maximum DB seg length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|--------|-------|--------|----------|--------------------|
| 1 | 2805 | 100.0 | 530 | 2 JCS939 | estrogen receptor |
| 2 | 2522 | 89.9 | 477 | 2 S71400 | estrogen receptor |
| 3 | 2284 | 81.4 | 503 | 2 JW0046 | estrogen receptor |
| 4 | 1230.5 | 43.9 | 589 | 1 QRCHE | estrogen receptor |
| 5 | 1224.5 | 43.7 | 595 | 1 QRHUE | estrogen receptor |
| 6 | 1219.5 | 43.5 | 595 | 2 I47140 | estrogen receptor |
| 7 | 1218.5 | 43.4 | 599 | 1 ORKSE | estrogen receptor |
| 8 | 1216.5 | 43.4 | 600 | 1 ORKTE | estrogen receptor |
| 9 | 1214 | 43.3 | 586 | 1 ORKLE | estrogen receptor |
| 10 | 1199 | 42.7 | 620 | 2 T10423 | estrogen receptor |
| 11 | 1174.5 | 41.9 | 701 | 2 S64737 | 80K estrogen recep |
| 12 | 1134.5 | 40.4 | 535 | 2 S58224 | estrogen receptor |
| 13 | 1120 | 39.9 | 574 | 2 A37197 | estrogen receptor |
| 14 | 631.5 | 22.5 | 433 | 2 B29345 | steroid hormone re |
| 15 | 619.5 | 22.1 | 433 | 2 S58087 | estrogen receptor |
| 16 | 597.5 | 21.3 | 521 | 2 A43345 | steroid hormone re |
| 17 | 471 | 16.8 | 467 | 2 A43781 | retinoid-X-recepto |
| 18 | 469.5 | 16.7 | 923 | 2 A39596 | progesterone recep |
| 19 | 465 | 16.6 | 923 | 2 I53280 | progesterone recep |
| 20 | 459 | 16.4 | 446 | 2 A34418 | H-2 region II bind |
| 21 | 459 | 16.4 | 451 | 2 A41651 | retinoic acid rece |
| 22 | 458.5 | 16.3 | 533 | 2 S37781 | retinoid X recepto |
| 23 | 457.5 | 16.3 | 758 | 2 S60586 | glucocorticoid rec |
| 24 | 456 | 16.3 | 448 | 2 A41727 | retinoid X recepto |
| 25 | 456 | 16.3 | 520 | 2 I84718 | RXR-beta1 isoform |
| 26 | 455.5 | 16.2 | 410 | 2 S28669 | retinoic acid rece |
| 27 | 453 | 16.1 | 948 | 2 JG0194 | androgen receptor |
| 28 | 453 | 16.1 | 930 | 2 A25923 | progesterone recep |
| 29 | 452 | 16.1 | 463 | 2 S26670 | retinoic acid rece |

RESULT 1
JCS939
estrogen receptor beta - human
C:Species: Homo sapiens (man)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JCS939
R:Ogawa, S.; Inoue, S.; Watanabe, T.; Hiroi, H.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Murai
Biochem. Biophys. Res. Commun. 243, 122-126, 1998
A>Title: The complete primary structure of human estrogen receptor beta (hERbeta) and
A:Reference number: JCS939; MUID:98139878; PMID:9473491
A:Accession: JCS939
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 530 <OGA>
A:Cross-references: DDBJ:AB06590; NID:G2911151; PID:BAA24953.1; PID:G2911152
C:Superfamily: estrogen receptor; ERBA transforming protein Homology
F:147-408/Domain: ERBA transforming protein homology <ERB>

| Query Match | 100.0% | Score 2805 | DB 2 | Length 530 |
|-----------------------|----------------|--|----------|------------|
| Best Local Similarity | 100.0% | Pred. No. 7.3e-211 | | |
| Matches 530 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| Qy | 1 | MDIKNSPSSNSPSSVNCQSLPLEHGSITIPSSVNSHHEYPAMTVPSPAMVNSIPS | 60 | |
| Db | 1 | MDIKNSPSSNSPSSVNCQSLPLEHGSITIPSSVNSHHEYPAMTVPSPAMVNSIPS | 60 | |
| Qy | 61 | NVTNLEGGPGRTTSPNVLWPTPGHLSPLVWHRQLSHLYASPQSPWCBAASLEHTLPVN | 120 | |
| Db | 61 | NVTNLEGGPGRTTSPNVLWPTPGHLSPLVWHRQLSHLYASPQSPWCBAASLEHTLPVN | 120 | |
| Qy | 121 | RETLKXKUSGNCASPVTPGSGKRDHFCVCSDVASGVHYGVNSCEGCKAFFKESIQGH | 180 | |
| Db | 121 | RETLKXKUSGNCASPVTPGSGKRDHFCVCSDVASGVHYGVNSCEGCKAFFKESIQGH | 180 | |
| Qy | 181 | NDYICPATNQCTIDKNRRKSCOACLRKCYEVMVKGSRRCRCYRLVRQRSADQLH | 240 | |
| Db | 181 | NDYICPATNQCTIDKNRRKSCOACLRKCYEVMVKGSRRCRCYRLVRQRSADQLH | 240 | |
| Qy | 241 | CAGKARSGGHPRVRELLLDALSPQLVLTLEAPPHVLISRPSPAPPTASMMMSLTK | 300 | |
| Db | 241 | CAGKARSGGHPRVRELLLDALSPQLVLTLEAPPHVLISRPSPAPPTASMMMSLTK | 300 | |
| Qy | 301 | LADKELVHMSWAKKIPGFVBLSLFDQVRLLESCHMEVLMGLMWRSIDHFGKLIAPDL | 360 | |
| Db | 301 | LADKELVHMSWAKKIPGFVBLSLFDQVRLLESCHMEVLMGLMWRSIDHFGKLIAPDL | 360 | |
| Qy | 361 | VDLRDGEKVEGILAIEMLLATTSRRELKLOHKEYLCVKAMILLNSMPLVTATODA | 420 | |
| Db | 361 | VDLRDGEKVEGILAIEMLLATTSRRELKLOHKEYLCVKAMILLNSMPLVTATODA | 420 | |
| Qy | 421 | DSSRLAHLLNAVTDALVWVIAKSGISSQQSMRLANILLMLSHVRHASNKGMEHLLNMK | 480 | |

Db 421 DSRKLAHLNNAVTDALVWVIAKSGISSQQSMELANLLMLLSHVHRASNKGMHLLNWK 480

Qy 481 CKNVVPPYDILLLEMLNAHVLRGCKSSITGSECPAEDSKSGSQNPQSQ 530

Db 481 CKNVVPPYDILLLEMLNAHVLRGCKSSITGSECPAEDSKSGSQNPQSQ 530

RESULT 2

S71400

estrogen receptor beta - human

C:Species: Homo sapiens (man)

C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Jun-2000

C:Accession: S71400

R:Mooselman, S.; Poelman, J.; Dijkema, R.

FEBS Lett. 392, 49-53, 1996

A:Title: ER-beta: identification and characterization of a novel human estrogen receptor

A:Reference number: S71400; MUID:96354875; PMID:8769313

A:Accession: S71400

A:Molecule type: mRNA

A:Residues: 1-477 <NOS>

A:Cross-references: EMBL:X99101; NID:g1518262; PIDN:CAA67555.1; PID:g1518263

C:Superfamily: estrogen receptor; erba transforming protein homology

C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor

F:94-355/Domain: erba transforming protein homology <ERBA>

F:96-116/Region: zinc finger CCCC motif

F:132-156/Region: zinc finger CCCC motif

F:167-182/Region: nuclear location signal

F:52/Binding site: phosphate (Ser) (covalent) (by MAP kinase) #status predicted

F:96,99,113,116/Binding site: zinc (Cys) #status predicted

F:132,138,148,151/Binding site: zinc (Cys) #status predicted

Query Match 89.9%; Score 2522; DB 2; Length 477;

Best Local Similarity 100.0%; Pred. No. 7.5e-189;

Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 MNYISPNVNLGGPGRQTTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPACEARSL 113

Db 1 MNYISPNVNLGGPGRQTTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPACEARSL 60

Qy 114 EHTLPVNRRLKRVKSGNRCASPVTPGSKRDAHFCAVCSYASGYHYGVMSCEGCKAFF 173

Db 61 EHTLPVNRRLKRVKSGNRCASPVTPGSKRDAHFCAVCSYASGYHYGVMSCEGCKAFF 120

Qy 174 KRISQGHNDYICPATNCTIDKNRKSQAACRLKCYEVGMVCKGSRRCRGYLRVRQR 233

Db 121 KRISQGHNDYICPATNCTIDKNRKSQAACRLKCYEVGMVCKGSRRCRGYLRVRQR 180

Qy 234 SADEQLHCAGKAKRSGCHAPVRRELLDALSPEQLVTLLEAEPHVLISRPSAPFTAS 293

Db 181 SADEQLHCAGKAKRSGCHAPVRRELLDALSPEQLVTLLEAEPHVLISRPSAPFTAS 240

Qy 294 MMSLTAKLADKELVEMISNAKKIPGVVELSLFDQVRLLESCHMEVLMMGLMWSRIDHPGK 353

Db 241 MMSLTAKLADKELVEMISNAKKIPGVVELSLFDQVRLLESCHMEVLMMGLMWSRIDHPGK 300

Qy 354 LI FAPDLVLRDRGKCEGILEIFDMLLATTSRPRELAKHKEYLCVKAMILLNSSMYPL 413

Db 301 LI FAPDLVLRDRGKCEGILEIFDMLLATTSRPRELAKHKEYLCVKAMILLNSSMYPL 360

Qy 414 VTATQADSRRLAHLLNAVTDALVWVIAKSGISSQQSMELANLLMLLSHVHRASNKGM 473

Db 361 VTATQADSRRLAHLLNAVTDALVWVIAKSGISSQQSMELANLLMLLSHVHRASNKGM 420

Qy 474 EHLNLMCKNVVPPYDILLLEMLNAHVLRGCKSSITGSECPAEDSKSGSQNPQSQ 530

Db 421 EHLNLMCKNVVPPYDILLLEMLNAHVLRGCKSSITGSECPAEDSKSGSQNPQSQ 477

RESULT 3

JW0046

estrogen receptor beta2 - rat

N:Alternate names: ERbeta2

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999

C:Accession: JW0046

R:Maruyama, K.; Endoh, H.; Sasaki-Iwaka, H.; Kanou, H.; Shimaya, E.; Hashimoto, S.; K. Biochem. Biophys. Res. Commun. 246, 142-147, 1998

A:Title: A novel isoform of rat estrogen receptor beta with 18 amino acid insertion in A:Reference number: JW0046; MUID:98262932; PMID:9600083

A:Accession: JW0046

A:Molecule type: mRNA

A:Residues: 1-503 <NAR>

A:Cross-references: DDBJ:AB012721

C:Comment: This protein functions as a negative regulator of estrogen action.

C:Superfamily: estrogen receptor; erba transforming protein homology

F:102-381/Domain: erba transforming protein homology <ERBA>

Query Match 81.4%; Score 2284; DB 2; Length 503;

Best Local Similarity 85.9%; Pred. No. 2.9e-170;

Matches 432; Conservative 23; Mismatches 30; Indels 18; Gaps 1;

Qy 46 MTEYSPAVNMYSTIPSNVTNLGGPGRQTTSPNVLPPTGHLSPVVRQLSHLYAEPOKS 105

Db 1 MTEYSPAVNMYSTIPSNVTNLGGPGRQTTSPNVLPPTGHLSPVVRQLSHLYAEPOKS 60

Qy 106 PWCEARSLRHTLPVNRRLKRVKSGNRCASPVTPGSKRDAHFCAVCSYASGYHYGVMS 165

Db 61 PWCEARSLRHTLPVNRRLKRVKSGNRCASPVTPGSKRDAHFCAVCSYASGYHYGVMS 120

Qy 166 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRKSQAACRLKCYEVGMVCKGSRRCRG 225

Db 121 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRKSQAACRLKCYEVGMVCKGSRRCRG 180

Qy 226 YRLVRQRSADEQLHCAGKAKRSGCHAPVRRELLDALSPEQLVTLLEAEPHVLISR 285

Db 181 YRLVRQRSADEQLHCAGKAKRSGCHAPVRRELLDALSPEQLVTLLEAEPHVLISR 240

Qy 286 SAPTEASMMMSITKLADKELVEMISNAKKIPGVVELSLFDQVRLLESCHMEVLMMGLM 345

Db 241 SAPTEASMMMSITKLADKELVEMISNAKKIPGVVELSLFDQVRLLESCHMEVLMMGLM 300

Qy 346 RSIDHPGKLI FAPDLVLRDRGKCEGILEIFDMLLATTSR 387

Db 301 RSIDHPGKLI FAPDLVLRDRGKCEGILEIFDMLLATTSR 360

Qy 388 RELKQHKVLCVKAMILLNSSMYPLVATQADSRRLAHLLNAVTDALVWVIAKSGIS 447

Db 361 RELKQHKVLCVKAMILLNSSMYPLASANQAESRKLTHLLNAVTDALVWVIAKSGIS 420

Qy 448 SQQSMRLANLLMLLSHVHRASNKGMHLLNMMCKNVVPPYDILLLEMLNAHVLRGCKSSI 507

Db 421 SQQSMRLANLLMLLSHVHRASNKGMHLLNMMCKNVVPPYDILLLEMLNAHVLRGCKSSI 480

Qy 508 TGSECPAEDSKSGSQNPQSQ 530

Db 481 TGSECPAEDSKSGSQNPQSQ 503

RESULT 4

ORCHE

estrogen receptor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999

C:Accession: A40914; S07182

R:Maxwell, B.D.; McDonnell, D.P.; Conneely, O.M.; Schulz, T.Z.; Greene, G.L.; O'Malley, M.J. Endocrinol. 1, 25-35, 1987

A:Title: Structural organization and regulation of the chicken estrogen receptor.

A:Reference number: A40914; MUID:88318621; PMID:2901032

A:Accession: A40914

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-589 <MAX>

R:Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P. EMBO J. 5, 891-897, 1986

A:Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oestrogen receptor.

A:Reference number: S07192; MUID:86247578; PMID:3755102

RESULT 5
QRRHUE
estrogen receptor 1 - human
N;Alternate names: ERL; estrogen receptor alpha
C.Species: Homo sapiens (man)
C.Date: 28-May-1986 #sequence,revision 28-May-1986 #text change 22-Jun-1999
C.Accession: A94284; A93376; A43021; S27143; S34000; A41925; B41935; A03244; C41925; D41

F:185-205/Region: zinc finger CCCC motif
F:221-245/Region: zinc finger CCCC motif
F:300-595/Domain: steroid binding #status predicted <STB>
F:236,305/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.7%; Score 1224.5; DB 1; Length 595;
Best Local Similarity 48.3%; Pred. No. 166-87;
Matches 263; Conservative 88; Mismatches 129; Indels 55; Gaps 14;

QY 5 NSPSSINSPSSVNCSCQILPLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAMVNYSPS 60
DB 21 NELEPLNRP-----QLKIPLERPLGEVYVDSS-----KPAVINYPEGAAY 74

QY 61 NVTNLEGGGRQ-----SIP-SNVTNLEGGGRQ-----TTSPNVLWPTPGHLSAP-LVHRSQLSHYAE 101
DB 75 Q-TGLPYGSGSAAAFSGNLGGFPPLNSVSPSLMLLHPPLQSPFLOPHGQVPPYLE 133

QY 102 POKSPWC--EARSLEHTLPVNRRETLKRVSGNRCASPVTPGP-----SKRDAHFCAVCS 154
DB 134 NEPSGVTVREAGPPAFYRP---NSDNRQGGRRERLASTNDKSGMAMESAKETRYCAVCD 190

QY 155 YASGHYGVWSCGCKAPFKRSIOGHNDYICPATNOCTIDKRRKSCCACRLKCYEVM 214
DB 191 YASGHYGVWSCGCKAPFKRSIOGHNDYICPATNOCTIDKRRKSCCACRLKCYEVM 250

QY 215 VKCGRRRCGRLVRRQRSADQLHCAGKAKRSQGHAPVR-----EL 258
DB 251 MKGGIRKORGGRLKHKQRDD----GEGRGVSGAGDMRAANLWPSPLMKRSKNS 305

QY 259 LLDALSPQGLVTLAEAPHVLSR--PSAPTEASMMSTLKLADKELVHMIWAKKI 316
DB 306 LALSUTADQWAGALLDAEPP--ILYSEYDTRFPLSEASMMGLLTNLADRELVHMIWAKRV 364

QY 317 PGFVELSLFDQVLLSCEMVEVLMMGLMWRSDHDPKLIJFAPDLVDRDEGKCVGILEI 376
DB 365 PGFVDTLHDQVHLLSCEMVEVLMMGLMWRSDHDPKLIJFAPDLVDRDEGKCVGILEI 424

QY 377 FMKLATTSRFRKLQHKYLCVKAMILLNSMPLVTAT--QDASRKLALHNAVTD 435
DB 425 FMKLATTSRFRFMNMQGEEFVCLKSIILNSGVYTFSLSTLKSLEKDHHRVLDKTD 484

QY 436 ALVWVIAKSGISSQQSQSMELANLLMLLSHVHSHASNGMEHLNMMKCNVVPVYDILLEL 495
DB 485 TIHLMAKAGLTLOQHQRLAQLLLLSHSHIRHWSNKGMEHLNMMKCNVVPVYDILLEL 544

QY 496 NAHVL 500
DB 545 DAHRL 549

RESULT 6
I47140
estradiol receptor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text_change 20-Aug-1999
C:Accession: I47140; S66250; S32402
R:Bokenkamp, D.; Jungblut, P.W.; Thole, H.H.
Mol. Cell. Endocrinol. 104, 163-172, 1994
A:Title: The C-terminal half of the porcine estradiol receptor contains no post-translat
A:Reference number: I47140; MUID:95080454; PMID:7988744
A:Accession: I47140
A:Status: preliminary; translated from GB/EXBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-595 <BOX>
A:Cross-references: EMBL:237167; NID:g587554; PIDN:CAA85524.1; PID:g587555
A:Experimental source: uterus
R:Thole, H.H.; Maschler, I.; Jungblut, P.W.
Eur. J. Biochem. 231, 510-516, 1995
A:Title: Surface mapping of the ligand-filled C-terminal half of the porcine estradiol r
A:Reference number: S66250; MUID:95361877; PMID:7635163
A:Accession: S66250
A:Molecule type: protein
A:Residues: 297-307;310-313;320-323;329-332;337-340;417-420;466-473 <THO>

A:Experimental source: uterus
R:Thole, H.H.
FEBS Lett. 320, 92-96, 1993
A:Title: Assignment of the ligand binding site of the porcine estradiol receptor to th
A:Reference number: S32402; MUID:93209384; PMID:8458437
A:Accession: S32402
A:Molecule type: Protein
A:Residues: 303-323 <TH>
A:Superfamily: estrogen receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transcript
F:1-120/Domain: amino-terminal <NH2>
F:121-299/Domain: DNA binding #status predicted <DNA>
F:183-456/Domain: erba transforming protein homology <ERBA>
F:185-205/Region: zinc finger CCCC motif
F:221-245/Region: zinc finger CCCC motif
F:256-271/Region: nuclear location signal
F:300-595/Domain: steroid binding #status predicted <STB>
F:185,188,202,205/Binding site: zinc (Cys) #status predicted
F:221,227,237,240/Binding site: zinc (Cys) #status predicted
F:236,305/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.5%; Score 1219.5; DB 2; Length 595;
Best Local Similarity 46.0%; Pred. No. 3.8e-87;
Matches 268; Conservative 89; Mismatches 126; Indels 99; Gaps 19;

QY 5 NSPSSINSPSSVNCSCQILPLEH--GSIYIPSSVVDHSHHEYPAMTFYSPAMVNY----- 56
DB 21 NELEPLNRP-----QLKIPLERPLGEVYVDSS-----KPAVINYPEGAAY 60

QY 57 -----SIP-SNVTNLEGGGRQ-----TTSPNVLWPTPGHLSAP- 88
DB 61 DFNAARASADVYQSGSLAYGPGSEAAAFANGLGQGPLNSVSPSLVLLHPPLQSPF 120

QY 89 LVHRSQLSHYAEPOKSPWC--EARSLEHTLPVNRRETLKRVSGNRCASPVTPGP----- 141
DB 121 LEPHGQVPPYLENEPSGYAVREAGPPAFYRP---NSDNRQGGRRERLASTDKSGMAME 177

QY 142 SKRDAHFCAVCSYASGHYGVWSCGCKAPFKRSIOGHNDYICPATNOCTIDKRRKSC 201
DB 178 SAKTRYCAVNDYASGHYGVWSCGCKAPFKRSIOGHNDYICPATNOCTIDKRRKSC 237

QY 202 QACRLKCYEVMKCGSRRCGRLVRRQRSADQLHCAGKAK-----RSGG-- 250
DB 238 QACRLKCYEVMKCGSRRCGRLVRRQRSADQLHCAGKAK-----GEGRNEAVPPGDMESANLW 292

QY 251 -----HAPVRELLLDALSPQGLVTLAEAPHVLSR--PSAPTEASMMSTLKL 301
DB 293 PSPLLIKHTKNSFVL--SLTADQMISALLEAEPP--IYSEYDTRFPLSEASMMGLLTNL 349

QY 302 ADKELVHMIWAKKI PGFVELSLFDQVLLSCEMVEVLMMGLMWRSDHDPKLIJFAPDLV 361
DB 350 ADRELVHMIWAKRVPGFVDTLHDQVHLLSCEMVEVLMMGLMWRSDHDPKLIJFAPDLV 409

QY 362 LDRDEGKCVGILEIFOMKLATTSRFRKLQHKYLCVKAMILLNSMPLVTAT--QDA 420
DB 410 LDRNQKCKVEGMVEIFOMKLATTSRFRFMNMQGEEFVCLKSIILNSGVYTFSLSTLKS 469

QY 421 DSSRKLALHNAVTDALVWVIAKSGISSQQSQSMELANLLMLLSHVHSHASNGMEHLNMMK 480
DB 470 BEKHDIHRVLDKTDITLHMAKAGLTLOQHQRLAQLLLLSHSHIRHWSNKGMEHLNMMK 529

QY 481 CNVVPVYDILLEMLNNAHVLRCGKSSITGSCSPAESKSK 522
DB 530 CNVVPVYDILLEMLNNAHVLRCGKSSITGSCSPAESKSK 567

RESULT 7
QRMSE
estrogen receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
C:Accession: A40061
R:White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.

Mol. Endocrinol. 1, 735-744, 1987
A;Title: Structural organization and expression of the mouse estrogen receptor.
A;Reference number: A40061; MID:91042558; PMID:2484714
A;Accession: A40061
A;Molecule type: mRNA
A;Residues: 1-599 <WH1>
A;Cross-references: GB:M38651; NID:G193179; PIDN:AAA37580.1; PID:G193180
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F;1-183/Domain: amino-terminal <NH2>
F;184-275/Domain: DNA binding #status predicted <DNA>
F;187-210/Region: zinc finger CCCC motif
F;223-245/Region: zinc finger CCCC motif
F;260-275/Region: nuclear location signal
F;304-556/Domain: steroid binding #status predicted <STB>
F;189,192,206,209/Binding site: zinc (Cys) #status predicted
F;225,231,241,244/Binding site: zinc (Cys) #status predicted
F;240,309/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.4%; Score 1218.5; DB 1; Length 599;
Best Local Similarity 45.8%; Pred. No. 4.6e-87;
Matches 263; Conservative 98; Mismatches 152; Indels 61; Gaps 14;

QY 5 NSPSSLSNPSYNSCSQILPLEH--GSIYIPSS--YVDSHHEYPAMTFYSPAVMYNYSIPS 60
Db 21 NLELEPLNRP-----QLKMPMERALGEVYVDSNKPVTENYPEGAAFEFNAAAAAAAGA 74

QY 61 NVTNLBEG---GPGRQ-----TTSNVLWPTFGHLSPL-LVHRQLSHL 98
Db 75 PVYQGSIAYGPGSEAAAFSANGSLGAPFQNLNSVSPFLMLHPPLSPFLPHGQGVY 134

QY 99 YASPOKSPWCEARSLHTLP---VNRRTLRKRVSGNRCAASPVTPGPG-----SKRDAHFA 150
Db 135 YLENEPS-----AVAVRTGTPPAPYRSNDRNGRERLSSNKGWIMESAKEYTCA 190

QY 151 VCSDYASGYHYGWSCEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQACRLRKCY 210
Db 191 VCNDYASGYHYGWSCEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQACRLRKCY 250

QY 211 EVGMVKGSRRRRCGYELVRRORSADP-----QLHCAGKAKRSG-----GHAPRVRE 257
Db 251 EVGMVKGSRRRRCGYELVRRORSADP-----QLHCAGKAKRSG-----GHAPRVRE 310

QY 258 LLLDALSPQLVLTLEAPPHVLIS-RPSAPFTEASMMVSLTKLADKELVHMISWAKKI 316
Db 311 AL--SLTADQVMSALDABPPMIYSEYDPSRPFSEASMMGLLTNLADRELVLHMNAKRV 368

QY 317 PGFVELSLFDQVRLLESCHWVLMGLMWSIDHPCKLIIFAPDLVLDSDGKCVGILEI 376
Db 369 PGFGLNLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLILLDRNOGKCVGMEI 428

QY 377 FDMLLATTSRPRELKLQHKVEYLCVKAMILLNSMYPVLVAT-ODADSRLKHLNAAVTD 435
Db 429 FDMLLATTSRPRMNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDHHRVLDKTD 488

QY 436 ALVWVIKSGISSQQQSNRLANILLMLSHVRHASKNGKMEHLNKKCNVPTDLLLEML 495
Db 489 TLIIHMAKAGLTLOOQHRLAQLLIILSHIRHMSNKGMEHLNKKCNVPTDLLLEML 548

QY 496 NAHVLRGCKSSITGSCSPADSKSKSGSNQPS 529
Db 549 DAHRLHAPARMGVPEEPSTQATLTTSSISAHS 582

RESULT 8
ORRTE
estrogen receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999

C;Accession: S07379; S16731
R;Koike, S.; Sakai, M.; Muramatsu, M.
Nucleic Acids Res. 15, 2499-2513, 1987
A;Title: Molecular cloning and characterization of rat estrogen receptor cDNA.
A;Reference number: S07379; MID:87174780; PMID:3031601
A;Accession: S07379
A;Molecule type: mRNA
A;Residues: 1-600 <KOI>
A;Cross-references: EMBL:Y00102; NID:G56110; PIDN:CAA68287.1; PID:G56111
R;Maggi, A.M.A.
submitted to the EMBL Data Library, June 1991
A;Reference number: S16731
A;Accession: S16731
A;Molecule type: mRNA
A;Residues: 1-487, 'T', 489-600 <MAG>
A;Cross-references: EMBL:X61098; NID:G56120; PIDN:CAA43411.1; PID:G56121
C;Comment: The steroid hormones and their receptors are involved in the regulation of e
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start si
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F;1-184/Domain: amino-terminal <NH2>
F;185-276/Domain: DNA binding #status predicted <DNA>
F;188-461/Domain: erba transforming protein homology <ERBA>
F;188-211/Region: zinc finger CCCC motif
F;224-246/Region: zinc finger CCCC motif
F;261-276/Region: nuclear location signal
F;305-557/Domain: steroid binding #status predicted <STB>
F;190,193,207,210/Binding site: zinc (Cys) #status predicted
F;226,232,242,245/Binding site: zinc (Cys) #status predicted
F;241,310/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.4%; Score 1216.5; DB 1; Length 600;
Best Local Similarity 45.7%; Pred. No. 6.6e-87;
Matches 262; Conservative 99; Mismatches 135; Indels 77; Gaps 17;

QY 5 NSPSSLSNPSYNSCSQILPLEH--GSIYIPSYVDSHHEYPAMTFY-----SPAVMYN 56
Db 21 NLELEPLNRP-----QLKMPMERALGEVYVDSN-KPAVFNYPGAAFEFNAAAAAAAGA 73

QY 57 STP-----SNVTNLBEGGPGRQ-----TTSNVLWPTFGHLSPLV---V 91
Db 74 SAPVYQGSSITY---GPGSEAAAFGANSGLGAPFQNLNSVSPFLMLHPPHVSPFLPHG 130

QY 92 HROLSHLYAEPQKSPWCEARSLHTLP---VNRRTLRKRVSGNRCAASPVTPGPG-----SK 143
Db 131 HQPYYLENEP-----SAYAVRTGTPPAPYRSNDRNGRERLSSSSEKGNWIMESA 184

QY 144 RDAHPCAVCSYASGYHYGWSCEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQA 203
Db 185 KETRYCAVCNDVASYGYHYGWSCEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQA 244

QY 204 CRLKCYEYGMVKGSRRRRCGYELVRRORSADP-----QLHCAGKAKRSG-----G 250
Db 245 CRLKCYEYGMVKGSRRRRCGYELVRRORSADP-----QLHCAGKAKRSG-----G 304

QY 251 HAPRVRELLDALSPQLVLTLEAPPHVLIS-RPSAPFTEASMMVSLTKLADKELVHM 309
Db 305 HTKKNSPAL--SLTADQVMSALDABPPMIYSEYDPSRPFSEASMMGLLTNLADRELVHM 362

QY 310 ISWAKKIPGFVELSLFDQVRLLESCHWVLMGLMWSIDHPCKLIIFAPDLVLDSDGK 369
Db 363 INWAKKIPGFGLNLHDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLILLDRNOGK 422

QY 370 VEGILBIFDMLLATTSRPRELKLQHKVEYLCVKAMILLNSMYPVLVAT-ODADSRLKLAH 428
Db 423 VEGWVEIFDMLLATTSRPRMNLQGEFVCLKSIILLNSGVYTFSLSTLSLEKDHHR 482

QY 429 LINAVTDALVWVIKSGISSQQQSNRLANILLMLSHVRHASKNGKMEHLNKKCNVPTV 488
Db 483 VLDKINDTLIIHMAKAGLTLOOQHRLAQLLIILSHIRHMSNKGMEHLNKKCNVPTV 542

QY 489 DILLEMLNAHVLRGCKSSITGSCSPADSKSK 521

Db 543 DILLEMLDAHLHAPASRM--GVPEEPSQSQ 572

RESULT 9
QXRLIE
estrogen receptor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 28-Feb-1992 #sequence_revision 14-Jul-1994 #text_change 15-Jun-1996
C:Accession: A40907
R:Weiler, I.J.; Lew, D.; Shapiro, D.J.
Mol. Endocrinol. 1, 355-362, 1987
A:Title: The Xenopus laevis estrogen receptor: sequence homology with human and avian re
A:Reference number: A40907; MUID:90331927; PMID:3274894
A:Accession: A40907
A:Molecule type: mRNA
A:Residues: 1-586 <WEI>
A:Cross-references: GB:L20735
C:Comment: In the steroid hormones and their receptors are involved in the regulation of eu
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C:Superfamily: estrogen receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F:1-174/Domain: amino-terminal <NH2>
F:175-266/Domain: DNA binding #status predicted <DNA>
F:178-448/Domain: erba transforming protein homology <ERBA>
F:178-201/Region: zinc finger CCCC motif
F:214-237/Region: zinc finger CCCC motif
F:251-266/Region: nuclear location signal
F:292-544/Domain: steroid binding #status predicted <STB>
F:180,183,197,200/Binding site: zinc (Cys) #status predicted
F:216,222,232,235/Binding site: zinc (Cys) #status predicted
F:233/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.3%; Score 1214; DB 1; Length 586;
Best Local Similarity 48.6%; Pred. No. 1e-86;
Matches 255; Conservative 82; Mismatches 138; Indels 50; Gaps 12;

Qy 36 YVDSH-----EYP-----AMTFYSPAMVNTSIPSNVNEGGGRCQT-----TSP 76
Db 43 YVENRTGIFNYPEGTTVDFAAAAAPVYSSASLSAASETFGSSLTGLHTLNNVPSP 102

Qy 77 NVLWPTGHLSPVLRH-QLSHLYAEPQKSPCEARSLEHTLPVNRRLTKRKVSNRCAS 135
Db 103 VVFLAKLPOLSPFIHHGQVYLYSEGGTFAVREAAPTF-YRSSDNRQRSGRMS 161

Qy 136 PVTGPG-----SKRDAHFCVCSYASGHYGVWSCEGKAPFKRSIQGHNDYICPATNQ 190
Db 162 SANDKGPSPSMTETRYCAVCSYASGHYGVWSCEGKAPFKRSIQGHNDYICPATNQ 221

Qy 191 CTIDNRRKSCQACRLKCYEVGMVKCGRRRCGYRLVRRORSADQLHCAGKAKRGSG 250
Db 222 CTIDNRRKSCQACRLKCYEVGMVKGGIRKDRGRLLKHQKBEQ-----EQKNDVD 276

Qy 251 HA-----PRVRELLD---ALSPEQLVLTLEAPPHVLISRPSP-APTFASMM 296
Db 277 PSEIRTAGIWNVPSVKMSKLSVLSITAEQLISALMEAEPTVSEHDSKPLSEASNM 336

Qy 297 SITKLADKELVHMSWAKKIPGVFVLSLFDQVRLLESQWMLMGLMWSRIDHPKLI 356
Db 337 LUTNLADRELVMINWAKKIPGVFVLTLDQVLLLECAWLSILWGLVWRSVHPGKUS 396

Qy 357 APDLVLDREDEKCVGEGILFIDMLLATTSPRFLKQHKYLCVKAMILLNSMYP 416
Db 397 APNLLDRNQRGCVGLVEIFDMLVTTATRFPMELRGEFICLSIILLNSGVYTFSS 456

Qy 417 TQDADSSRLAH-LANAVTDALVWIAKSGISSQCSQKMLANMLLMLSHVHSHASNK 475
Db 457 TLESLEDTLIIHIIKDIITLVHMAKSGSLQOQOQRLAQQLLILSHIRMSNKGMEH 516

Qy 476 LLMKCNKVVVYDILLEMLNARHLRGCKSSITGSECSPAEDSKS 520
Db 517 LYSMKCNKVVVYDILLEMLDAHRIHTPKDKTTQGE-----EDSRS 557

RESULT 10
T10423
estrogen receptor - Oryzias sp. (strain d-rR)
C:Species: Oryzias sp.
A:Variety: strain d-rR
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T10423
R:Okada, H.; Kawahara, T.; Yamashita, I.
submitted to the EMBL Data Library, March 1994
A:Description: Cloning of medaka estrogen receptor cDNA.
A:Reference number: Z17013
A:Accession: T10423
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-620 <OKA>
A:Cross-references: EMBL:D28954
A:Experimental source: strain d-rR, liver
C:Genetics:
C:Gene: MER
C:Superfamily: estrogen receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation
P:184-460/Domain: erba transforming protein homology <ERB>

Query Match 42.7%; Score 1199; DB 2; Length 620;
Best Local Similarity 48.1%; Pred. No. 1.ee-85;
Matches 265; Conservative 81; Mismatches 129; Indels 76; Gaps 16;

Qy 36 YVDSHHEY-----PAMT-----FYSPAMVNTSIPS--NVTNLEGGGRCQTTPNVILW 80
Db 62 FLECTYDYAANPATTPLYSSOSTGYVSAPLETNGPPESEGLSGLSGSP-----TSPLVFV 117

Qy 81 PTPGHLSPVLRHQLSHLYAEPQKSPCEARSLEHTLPVNRRLTKRKVSGNR----CASPV 137
Db 118 PSSPRLSPFM--HPPSHLYLETTTTPVYRSS-----HQGASREDCQSSREDCSLGE 167

Qy 138 TPGCS-----KRDHFCVCSYASGHYGVWSCEGKAPFKRSIQGHNDYICPATNQ 190
Db 168 LGAGAGAGGEMAKDTFCVCSYASGHYGVWSCEGKAPFKRSIQGHNDYICPATNQ 227

Qy 191 CTIDNRRKSCQACRLKCYEVGMVKCGRRRCGYRLVRRQR-----SAD 236
Db 228 CTIDNRRKSCQACRLKCYEVGMVKGGVRKDR--IRLRDRKRTGVGDGVKVGQEH 285

Qy 237 EQLHCAGKAKES--GGHAPRVRELLDALSPQLVLTLEAPPHVLISRP--SAPFTEA 292
Db 286 KTVHYDGRKSSSTGGGGGGGGRSLVTSIPPEQVLLLLQGAEP--ILCSQKLSRPTEV 344

Qy 293 SMMSLTLKLADKELVHMSWAKKIPGVFVLSLFDQVRLLESQWMLMGLMWSRIDHPG 352
Db 345 TMTLTSMDKELVHMSWAKKIPGVFVLSLFDQVRLLESQWMLMGLMWSRIDHPG 404

Qy 353 KLIPAPDLVLDREDEKCVGEGILFIDMLLATTSPRFLKQHKYLCVKAMILLNSMYP 412
Db 405 KLIPAPDLVLDREDEKCVGEGILFIDMLLATTSPRFLKQHKYLCVKAMILLNSMYP 464

Qy 413 LVTATQD--ADSSRLAH-LANAVTDALVWIAKSGISSQCSQKMLANMLLMLSHVHSHASNK 471
Db 465 FCTGTMEPLHNSAAVQSMLOTITDALHYISQSYLAQEQARRQAQLLLSHIRMSNKG 524

Qy 472 GMEHLNKKCNKVVVYDILLEMLNARHLRGCKSSITGSECSPAE 516
Db 525 GMEHLNKKCNKVVVYDILLEMLDAHRIHTPKDKTTQGE-----SITGSECSPAE 584

Qy 517 DSKSKEGSONP 527
Db 585 ISASRGRIESP 595

RESULT 11
S64737
80K estrogen receptor - human

C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C;Accession: S64737
R;Pink, J.J.; Wu, S.Q.; Wolf, D.M.; Bilimoria, M.M.; Jordan, V.C.
Nucleic Acids Res. 24, 962-969, 1996
A;Title: A novel 80 kDa human estrogen receptor containing a duplication of exons 6 and 7
A;Reference number: S64737; MUID:96174665; PMID:8600466
A;Accession: S64737
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-701 <PIN>
A;Cross-references: EMBL:U47678; NID:91197854; PIDN:AAB00115.1; PID:91197855
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F;183-456/Domain: erba transforming protein homology #status atypical <ERBA>
F;518-562/Domain: erba transforming protein homology #status atypical <ERB2>

Query Match 41.9%; Score 1174.5; DB 2; Length 701;
Best Local Similarity 41.2%; Pred. No. 1.5e-83;
Matches 268; Conservative 87; Mismatches 125; Indels 171; Gaps 16;

Qy 5 NSPSLSPSYNSQSIPLPEH--GSIYIPSS--YDSHHEYPAMTFYSPAVNHYIPS 60
Db 21 NELEPLNR-----OLKIPLERPLGEVYLDSSRPVNYNPEGAAYEFNAAAAAQAQVYG 74
Qy 61 NVTNLEGGPGRQ-----TTSNVLWPTPGHLSPL-LVHROLSHLYAE 101
Db 75 Q-TCLPTGPGSEAAAFSGNLGGFPPLNSVSPSLMLHPPQLSPFLOPHGQVPPYLE 133
Qy 102 PQKSPWC--EARSLEHTLPVNRRETLKRVKSGNRCASPVTPGG-----SKDAHPACVSD 154
Db 134 NEPSGYTVREAGPAPFYRP--NSDNRQGGRRRLASTNDKGSMAESAKETRYCAVCD 190
Qy 155 YASGYHYGVMSCECKAPFKRSIOGHNDYICPATNCTIDKNRKSQACRLKCYEVGM 214
Db 191 YASGYHYGVMSCECKAPFKRSIOGHNDYICPATNCTIDKNRKSQACRLKCYEVGM 250
Qy 215 VKCSRRERCQYLRVRQRSADEQLHCAGKAKRSQGHAPVR-----EL 258
Db 251 MKGGRIRDRGRMLKHKRQRDD-----GEGRGVGSAGDMRAANLWPSPLMIKRSKNS 305
Qy 259 LLDALSPQLVLTLEAEPPHVLISR--PSAPTEASMMSLTKLADKELVHMSWAKKI 316
Db 306 LAUSLTADQVSAALDAEPP--ILSYDYDTPRPPEASMGLLTMDARELVEHINNAKRV 364
Qy 317 PGFVELSLFOVRLLESQWELMGLMWSIDHPGKLIIPAPDLVLDRECKCVGILEI 376
Db 365 PGFVDTLHDQVHLLCANLEIMGLVWRSMEHPVKLLFAPNLLDRNQGCKVGVVEI 424
Qy 377 FDMLLATSPRELKQHKYELCVKAMILLNSMYPLVAT-----QD----- 419
Db 425 FDMLLATSSRFRMNLQGEFVCLKSIILLNSGYTFLSSTLSLEBKDHHRVLDKTD 484
Qy 420 -----ADSSR----- 424
Db 485 TLHLMKAGLTQQQORLAQLLLSHIRHMRNQGCKVGVVEIFDMLLATSSRFRM 544
Qy 425 -----KLAHLINAVTDALVWVIKSGISSQ 449
Db 545 NLQGEFPVCLKSIILLNSGYTFLSSTLSLEBKDHHRVLDKTDTLHLMKAGLTQ 604
Qy 450 QQSMRLANLLMLSHVHASNKGMEHLNKKCKQVVPYDILLEMNAHVL 500
Db 605 QQHQRLAQLLLSHIRHMRNKGMEHLYSMKCKQVVPYDILLEMNAHVL 655

RESULT 12
S58224
oestrogen receptor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
C;Accession: S58224

R;Rogers, S.A.; Llewellyn, L.; Ramsurn, V.P.; Sweeney, G.E.; Wigham, T.
submitted to the EMBL Data Library, July 1995
A;Reference number: S58224
A;Accession: S58224
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-535 <ROG>
A;Cross-references: EMBL:X89959; NID:929901; PIDN:CAA61999.1; PID:929902
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F;103-382/Domain: erba transforming protein homology <ERBA>

Query Match 40.4%; Score 1134.5; DB 2; Length 535;
Best Local Similarity 48.8%; Pred. No. 1.4e-80;
Matches 246; Conservative 73; Mismatches 114; Indels 71; Gaps 15;

Qy 70 GROTTSNVLWPTPGHLSPLVHROLSH-----LYAEPKSPWCARSLEHTLPVNRRET 123
Db 17 GSSPTGLVFSVSSPOLSPF-LHPPGHGLPLOSYYLETSTPLYSVVVTLNLSAEE- 74
Qy 124 LKRVKSGNRCAS-PVTGPGSK-----RDAHFCAVCSDIASGYHYGVMSCEGCKAFFKRSI 177
Db 75 -KLCITSNQQSVAAAGSGVRVPEMANETRYCAVCSDFASGYHYGVMSCEGCKAFFKRSI 133
Qy 178 QGHNDYICPATNCTIDKNRKSQACRLKCYEVGMVKGSRRCGVLVVRQRSADE 237
Db 134 QGHNDYICPATNCTIDKNRKSQACRLKCYEVGMVKGSLKDR--GGRVLRK-----D 187
Qy 238 QLHC--AGKAKR-----SGGH-----APVRELLDALSPLOL 268
Db 188 KRYCGPAGDREKPYGDEHRTAPPDGGRRNSSSSSUSGGGCGCPRI-----TMPPEQV 241
Qy 269 VITLLBAEPPHVLISRPP--SAPTEASMMSLTKLADKELVHMSWAKKI PGFVELSLFD 326
Db 242 LFLQGAEP-ALCSRKQVARPYETVMTLLTSMADKELVHMIANAKVPGFOELSLHD 300
Qy 327 QVRLLESQWELMGLMWSIDHPGKLIIPAPDLVLDRECKCVGILEIFDMLLATTSR 386
Db 301 QVQLLESQWELMGLMWSIDHPGKLIIPAPDLVLDRECKCVGMAEIPDMLLATVSR 360
Qy 387 FRELKQHKYELCVKAMILLNSMYPLVT-ATODADSSRLKLAHLINAVTDALVWVIKSG 445
Db 361 FRLMLKLPBEFFVCKAIIILNSGAPSCNSVESLHNSAVESMLNDITDALIHSHSG 420
Qy 446 ISSQQSMRLANLLMLSHVHASNKGMEHLNKKCKQVVPYDILLEMNAHVLGRCKS 505
Db 421 ASVQQQPRQVQVQLLLSHIRHMRNKGMEHLYSIKCKVPLVYDLELLEMLDGHRLQ 476
Qy 506 SITGSCSPAEBSKSKSGSQNPQS 529
Db 477 -----SPKVAQAGEQTEGPF 493

RESULT 13
A37197
estrogen receptor - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999
C;Accession: A37197; A40070
R;Pakdel, F.; Le Gac, F.; Le Goff, P.; Valotaire, Y.
Mol. Cell. Endocrinol. 71, 195-204, 1990
A;Title: Full-length sequence and in vitro expression of rainbow trout estrogen receptor
A;Reference number: A37197; MUID:91006824; PMID:2210031
A;Accession: A37197
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-574 <PAK>
A;Cross-references: GB:M31559
R;Pakdel, F.; Le Guellec, C.; Vaillant, C.; Le Roux, M.G.; Valotaire, Y.
Mol. Endocrinol. 3, 44-51, 1989
A;Title: Identification and estrogen induction of two estrogen receptors (ER) messenger
A;Reference number: A40070; MUID:89127284; PMID:2915848
A;Accession: A40070

Qy 441 IAKSGISSQQQSVRLANLMLLSHVRHASNKGMEHLINMKCKNVVPVYDILLLEMLNAHV 499
Db 380 -----SORHEEPRRAGKLIWTLPLLRCTAAKAVQHPFYSVKLQCKVPWHLFLEMLEAKV 433

Search completed: June 20, 2004, 10:39:11
Job time : 22 secs

| Result No. | Score | Query Match | Length | DB | ID | Description | |
|------------|--------|-------------|--------|----|------------|-------------|--------------|
| | | | | | | | |
| 1 | 2805 | 100.0 | 530 | 1 | ESR2_HUMAN | Q92731 | homo sapien |
| 2 | 2615 | 93.2 | 530 | 1 | ESR2_CALJA | Q95171 | callithrix |
| 3 | 2496 | 89.0 | 530 | 1 | ESR2_RAT | Q62986 | rattus norv |
| 4 | 2495 | 88.9 | 530 | 1 | ESR2_MOUSE | Q08537 | mus musculus |
| 5 | 2463 | 87.8 | 527 | 1 | ESR2_BOVIN | Q9xsb5 | bos taurus |
| 6 | 2455.5 | 87.5 | 527 | 1 | ESR2_SHEEP | Q9tul5 | ovis aries |
| 7 | 2415 | 86.1 | 526 | 1 | ESR2_PIG | Q9xsw2 | sus scrofa |
| 8 | 2101 | 74.9 | 554 | 1 | ESR2_STUVU | Q9pve2 | sturnus vul |
| 9 | 1959 | 69.8 | 472 | 1 | ESR2_COTJA | Q93511 | coturnix co |
| 10 | 1948.5 | 69.5 | 472 | 1 | ESR2_CHICK | Q9ptu5 | gallus gall |
| 11 | 1549 | 55.2 | 573 | 1 | ESR2_ANGJA | Q13012 | anguilla ja |
| 12 | 1466 | 52.3 | 568 | 1 | ERB1_CARAU | Q9w669 | carassius a |
| 13 | 1440.5 | 51.4 | 568 | 1 | ESR2_ONCMY | P57782 | oncorhynch |
| 14 | 1431 | 51.0 | 673 | 1 | ESR2_MICUN | P57781 | micropogon |
| 15 | 1398 | 49.8 | 279 | 1 | ESR2_MACMU | Q9tte5 | macaca mlla |
| 16 | 1385.5 | 49.4 | 559 | 1 | ESR2_SPAAU | Q9w6m2 | sparus auru |
| 17 | 1381 | 49.2 | 575 | 1 | ESR2_ITCPU | Q9iak1 | ictalurus p |
| 18 | 1378.5 | 49.1 | 610 | 1 | ERB2_CARAU | Q9ial9 | carassius a |
| 19 | 1373 | 48.9 | 565 | 1 | ESR3_MICUN | P57783 | micropogon |
| 20 | 1352 | 48.2 | 557 | 1 | ESR2_ORENI | Q9ybh3 | oreochromis |
| 21 | 1333.5 | 44.0 | 585 | 1 | ESR1_HUMAN | P01372 | homo sapien |
| 22 | 1228.5 | 43.8 | 587 | 1 | ESR1_POEGU | Q91250 | poephila gu |
| 23 | 1225.5 | 43.7 | 589 | 1 | ESR1_CHICK | P06212 | gallus gall |
| 24 | 1220 | 43.5 | 594 | 1 | ESR1_HORSE | Q9tv98 | equus cabal |
| 25 | 1219.5 | 43.5 | 595 | 1 | ESR1_PIG | Q29040 | sus scrofa |
| 26 | 1219 | 43.5 | 595 | 1 | ESR1_MESAU | Q9qzj5 | mesocricetu |
| 27 | 1218.5 | 43.4 | 599 | 1 | ESR1_MOUSE | P19785 | mus musculu |
| 28 | 1216.5 | 43.4 | 600 | 1 | ESR1_RAT | P06211 | rattus norv |
| 29 | 1214 | 43.3 | 583 | 1 | ESR1_ORENI | Q9ybh3 | oreochromis |
| 30 | 1214 | 43.3 | 586 | 1 | ESR1_XENLA | P48559 | xenopus lae |
| 31 | 1210 | 43.1 | 569 | 1 | ESR1_BNARE | P57717 | brachydanio |
| 32 | 1204 | 42.9 | 579 | 1 | ESR1_SPAAU | Q9pvez9 | sparus auru |
| 33 | 1199 | 42.7 | 620 | 1 | ESR1_ORYLA | P50241 | oryzias lat |

CC TISSUE-Ovary;
 CC MEDLINE=98346389; PubMed=9685228;
 CC Lu B., Leygue E., Detzlaw H., Murphy L.J., Murphy L.C., Watson P.H.;
 CC "Estrogen receptor-beta mRNA variants in human and murine tissues.";
 CC Mol. Cell. Endocrinol. 138:199-203(1998).
 CC [7]
 CC RY SEQUENCE 1-69 FROM N.A.
 CC Li L.C., Dahiya R.;
 CC "Cloning and characterization of the estrogen receptor beta gene
 CC promoter.";
 CC J. Biol. Chem. 272:25832-25838(1997).
 CC [8]
 CC CHARACTERIZATION.
 CC MEDLINE=97467383; PubMed=9325313;
 CC Pace P., Taylor J., Suntharalingam S., Coombes R.C., Ali S.;
 CC "Human estrogen receptor beta binds DNA in a manner similar to and
 CC dimerizes with estrogen receptor alpha.";
 CC J. Biol. Chem. 272:25832-25838(1997).
 CC [9]
 CC INTERACTION WITH NCOA3.
 CC MEDLINE=97410121; PubMed=9267036;
 CC Chen H., Lin R.J., Schiltz R.L., Chakravarti D., Nash A., Nagy L.,
 CC Privalsky M.L., Nakatani Y., Evans R.M.;
 CC "Nuclear receptor coactivator ACTR is a novel histone
 CC acetyltransferase and forms a multimeric activation complex with P/CAP
 CC and CBP/p300.";
 CC Cell 90:569-580(1997).
 CC [10]
 CC INTERACTION WITH NCOA6.
 CC MEDLINE=20148724; PubMed=10681503;
 CC Calra F., Antonson P., Pellico-Huikko M., Treuter E., Gustafsson J.-A.;
 CC "Cloning and characterization of RAP250, a nuclear receptor
 CC coactivator.";
 CC J. Biol. Chem. 275:5308-5317(2000).
 CC [11]
 CC INTERACTION WITH NCOA5.
 CC MEDLINE=20565767; PubMed=11113208;
 CC Sauve F., McBreem L.D.B., Gallant J., Moraitis A.N., Labrie P.,
 CC Guigne V.;
 CC "CRA, a novel estrogen receptor coactivator with a bifunctional
 CC nuclear receptor interacting determinant.";
 CC Mol. Cell. Biol. 21:343-353(2001).
 CC -!- FUNCTION: Nuclear hormone receptor. Binds estrogens with an
 CC affinity similar to that of ESR1, and activates expression of
 CC reporter genes containing estrogen response elements (ERE) in an
 CC estrogen-dependent manner. Isoform beta-2 lacks ligand binding
 CC ability and has no or only very low binding activity resulting
 CC in the loss of ligand-dependent transactivation ability. DNA-
 CC binding by ESR1 and ESR2 is rapidly lost at 37 degrees Celsius in
 CC the absence of ligand while in the presence of 17 beta-estradiol
 CC and 4-hydroxy-tamoxifen loss in DNA-binding at elevated
 CC temperature is more gradual.
 CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
 CC ESR1. Isoform beta-2/cx preferentially forms a heterodimer with
 CC ESR1 rather than ESR2 and inhibits DNA-binding by ESR1. Interacts
 CC with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong
 CC increase of transcription of target genes.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=8;
 CC Name=1; Synonyms=Beta-1;
 CC IsoId=Q92731-1; SequencesDisplayed;
 CC Name=2; Synonyms=Beta-2, CX;
 CC IsoId=Q92731-2; Sequences=VSP_003689;
 CC Name=3; Synonyms=Beta-2A;
 CC IsoId=Q92731-3; Sequences=VSP_003684, VSP_003686;
 CC Name=4; Synonyms=Beta-3;
 CC IsoId=Q92731-4; Sequences=VSP_003690;
 CC Name=5; Synonyms=Beta-4;
 CC IsoId=Q92731-5; Sequences=VSP_003691;
 CC Name=6; Synonyms=Beta-5;
 CC IsoId=Q92731-6; Sequences=VSP_003692;
 CC Name=7; Synonyms=Beta-5A;
 CC IsoId=Q92731-7; Sequences=VSP_003685;
 CC Name=8; Synonyms=Beta-6;
 CC IsoId=Q92731-8; Sequences=VSP_003687, VSP_003688;
 CC TISSUE SPECIFICITY: Isoform beta-1 is expressed in testis and
 CC ovary, and at a lower level in heart, brain, placenta, liver,
 CC skeletal muscle, spleen, thymus, prostate, colon, bone marrow, and
 CC mammary gland and uterus. Also found in uterine bone, breast, and
 CC ovarian tumor cell lines, but not in colon and liver tumors.
 CC Isoform beta-2 is expressed in spleen, thymus, testis and ovary
 CC and at a lower level in skeletal muscle, prostate, colon, small
 CC intestine, leukocytes, bone marrow, mammary gland and uterus.
 CC Isoform beta-3 is found in testis. Isoform beta-4 is expressed in
 CC testis, and at a lower level in spleen, thymus, ovary, mammary
 CC gland and uterus. Isoform beta-5 is expressed in testis, placenta,
 CC skeletal muscle, spleen and leukocytes, and at a lower level in
 CC heart, lung, liver, kidney, pancreas, thymus, prostate, colon,
 CC small intestine, bone marrow, mammary gland and uterus. Not
 CC expressed in brain.
 CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
 CC a DNA-binding domain and a C-terminal steroid-binding domain.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
 CC subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@isb-sib.ch.
 CC -----
 CC EMBL; AB006590; BAA24953.1; -
 CC EMBL; AF051427; AAC05985.1; -
 CC EMBL; AF051428; AAC05951.1; -
 CC EMBL; AF061054; AAC39784.1; -
 CC EMBL; AF061055; AAC39785.1; -
 CC EMBL; AF060555; AAC15234.1; -
 CC EMBL; X99101; CAA67555.1; ALT_INIT.
 CC EMBL; AB006589; BAA31966.1; -
 CC EMBL; AF074598; AAC25602.1; -
 CC EMBL; AF074599; AAC25603.1; -
 CC EMBL; AF124790; AAC32580.1; -
 CC EMBL; AF07463; AAC3786.1; -
 CC EMBL; AF191544; AAF24232.1; -
 CC PDB; 1L2J; 01-MAY-02.
 CC PDB; 1NDE; 18-DEC-02.
 CC PDB; 1QKW; 28-JUL-00.
 CC TRANSFAC; T04651; -
 CC TRANSFAC; T05387; -
 CC TRANSFAC; T05388; -
 CC TRANSFAC; T05389; -
 CC TRANSFAC; T05390; -
 CC TRANSFAC; T05391; -
 CC Gene; HGNC:3469; ESR2.
 CC MIM; 601663; -
 CC GO; GO:0005634; C:nucleus; TAS.
 CC GO; GO:00030284; P:estrogen receptor activity; TAS.
 CC GO; GO:0048019; P:receptor antagonist activity; NAS.
 CC GO; GO:0005496; P:steroid binding; TAS.
 CC GO; GO:0003700; P:transcription co-activator activity; TAS.
 CC GO; GO:0003713; P:transcription factor activity; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0030520; P:estrogen receptor signaling pathway; TAS.
 CC GO; GO:0030308; P:negative regulation of cell growth; NAS.
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
 CC GO; GO:0007155; P:signal transduction; TAS.
 CC InterPro; IPR000536; Hormone_rec_lig.
 CC InterPro; IPR001723; Steroid_receptor.
 CC InterPro; IPR008946; Str_ncl_receptor.
 CC InterPro; IPR001628; Znf_C4steroid.
 CC Pfam; PF00104; hormone_rec; 1.
 CC Pfam; PF00105; zf-C4; 1.
 CC PRINTS; PR00398; STERHORMONER.

DB 361 IDRDGKCVGILVFMFLATTSFRFELKQHEYLVCVAMVLLNSQYDPLVATQDA 420
QY 421 DSSKRLAHLNVAITDALVWVIAKSGISQOQSMRLANILLSHVRHASNKGMEHLNMX 480
DB 421 BSSQKLAHLNVAITDALVWVIAKSGISQOQSVRLANILLSHVRHASNKGMEHLNMX 480
QY 481 CKNVVFVYDILLEMNAHVLGCKSKSITGSCSPAESKSGEGSONPOS 529
DB 481 CKNVVFVYDILLEMNAHVLGCKSKSITGSCSPAESKSGEGSONPOS 529
RESULT 3
ESR2 RAT STANDARD; PRT: 530 AA.
ID Q62986; O35784; O35785; O55015; O55016; O70195; Q9R185;
AC 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DI 10-OCT-2003 (Rel. 42, Last annotation update)
DE Estrogen receptor beta (ER-beta).
GN ESR2 OR NR3A2 OR ERBETA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 46-530 FROM N.A. (ISOFORM 1).
RC STRAIN=Sprague-Dawley; TISSUE=Prostate;
RX MEDLINE=96234066; PubMed=8650195;
RA Maruyama K., Endoh H., Sasaki-Iwacka H., Kanou H., Shimaya E.,
RA Hashimoto S., Kato S., Kawashima H.;
RT "A novel isoform of rat estrogen receptor beta with 18 amino acid
RT insertion in the ligand binding domain as a putative dominant
RT negative regulator of estrogen action".
RL Biochem. Biophys. Res. Commun. 246:142-147(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=Wistar; TISSUE=Ovary;
RX MEDLINE=96262932; PubMed=9600083;
RA Maruyama K., Endoh H., Sasaki-Iwacka H., Kanou H., Shimaya E.,
RA Hashimoto S., Kato S., Kawashima H.;
RT "A novel isoform of rat estrogen receptor beta with 18 amino acid
RT insertion in the ligand binding domain as a putative dominant
RT negative regulator of estrogen action".
RL Biochem. Biophys. Res. Commun. 246:142-147(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=Wistar; TISSUE=Prostate;
RX MEDLINE=96262932; PubMed=9600083;
RA Maruyama K., Endoh H., Sasaki-Iwacka H., Kanou H., Shimaya E.,
RA Hashimoto S., Kato S., Kawashima H.;
RT "A novel isoform of rat estrogen receptor beta with 18 amino acid
RT insertion in the ligand binding domain as a putative dominant
RT negative regulator of estrogen action".
RL Biochem. Biophys. Res. Commun. 246:142-147(1998).
RN [3]
RP SEQUENCE OF 46-530 FROM N.A. (ISOFORMS 1, 3 AND 4).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98151005; PubMed=9492041;
RA Petersen D.N., Thalcevic G.T., Kozar-Taylor P.H., Turi T.G.,
RA Brown T.A.;
RT "Identification of estrogen receptor beta2, a functional variant of
RT estrogen receptor beta expressed in normal rat tissues.";
RL Endocrinology 139:1082-1092(1998).
RN [5]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 5).
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Price R., Handa R.J.;
RT "A novel splice variant of estrogen receptor beta found in rat
RT brain.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Binds estrogens with an affinity similar to that of ER-
CC ALPHA, and activates expression of reporter genes containing
CC estrogen response elements (ERE) in an estrogen-dependent manner.
CC Isoform 3 and isoform 4 are unable to bind DNA and activate
CC transcription due to the truncation of the DNA binding domain.
CC Isoform 2 shows loss of ligand binding affinity and suppresses ER-

ALPHA and ER-BETA mediated transcriptional activation and may act
-!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
ESR1. Can also form heterodimers with isoforms 1 and 2.
CC Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a
CC strong increase of transcription of target genes (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=Beta1;
CC IsoId=Q62986-1; Sequence=Displayed;
CC Name=2; Synonyms=Beta2;
CC IsoId=Q62986-2; Sequence=VSP_003699;
CC Name=3; Synonyms=Beta2-delta3; Sequence=VSP_003697;
CC IsoId=Q62986-3; Sequence=VSP_003697;
CC Name=4; Synonyms=Beta2-delta3;
CC IsoId=Q62986-4; Sequence=VSP_003697; VSP_003699;
CC Name=5; Synonyms=Beta1-delta4;
CC IsoId=Q62986-5; Sequence=VSP_003698;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, OVARY, LIVER,
CC KIDNEY, FAT, BONE, BRAIN, UTERUS AND TESTIS.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EXBL: U57439; AAC52602.1; -
CC EXBL: AB012721; BAA25431.1; -
CC EXBL: AJ002602; CAA05631.1; ALT_INIT.
CC EXBL: AJ002603; CAA05632.1; -
CC EXBL: AF042058; AAB97424.1; -
CC EXBL: AF042059; AAB97425.1; -
CC EXBL: AF042060; AAB97426.1; -
CC EXBL: AF042061; AAB97427.1; -
CC EXBL: AF161187; AAD47637.1; -
CC PDB: 1HJ1; 04-JAN-02.
CC PDB: 1QKN; 28-JUL-00.
CC GO: GO:0005634; C:nucleus; ISS.
CC GO: GO:0030284; F:estrogen receptor activity; ISS.
CC GO: GO:0004879; F:ligand-dependent nuclear receptor activity; ISS.
CC GO: GO:0048019; F:receptor antagonist activity; ISS.
CC GO: GO:0035496; P:steroid binding; ISS.
CC GO: GO:0030520; P:estrogen receptor signaling pathway; ISS.
CC GO: GO:0030308; P:negative regulation of cell growth; ISS.
CC GO: GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
CC InterPro: IPR00536; Hormone_rec_lig.
CC InterPro: IPR001723; Steroid_receptor.
CC InterPro: IPR008946; Str_ncl_receptor.
CC InterPro: IPR01628; Znf_C4steroid.
CC Pfam: PF00104; hormone_rec; 1.
CC Pfam: PF00105; zf-C4; 1.
CC PRINTS: PR00398; STRDHORMONER.
CC PRINTS: PR000035; Znf_C4steroid; 1.
CC ProDom: PD000035; Znf_C4steroid; 1.
CC SMART: SM00399; Znf_C4; 1.
CC PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Steroid-binding; Alternative splicing; Phosphorylation;
CC 3D-structure.
FT DOMAIN 1 148 MODULATING.
FT DNA_BIND 149 214 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 149 169 C4-TYPE.
FT ZN_FING 185 209 C4-TYPE.
FT

| | | | | |
|---------------------------|--|---------------------|--|--|
| FT | DOMAIN | 215 | 530 | STERIOD-BINDING. |
| FT | MOD_RES | 87 | | PHOSPHORYLATION (BY SIMILARITY). |
| FT | MOD_RES | 488 | | PHOSPHORYLATION (BY SIMILARITY). |
| FT | VARSPLIC | 179 | 217 | Missing (in isoform 3 and isoform 4). |
| FT | | | | /FTid=VSP 003697. |
| FT | VARSPLIC | 219 | 318 | Missing (in isoform 5). |
| FT | | | | /FTid=VSP 003698. |
| FT | VARSPLIC | 364 | 364 | R -> RSSEDPHHVAQMSAADR (in isoform 2 and isoform 4). |
| FT | | | | /FTid=VSP 003699. |
| FT | CONFLICT | 72 | | L -> Q (IN REF. 3 AND 4). |
| FT | CONFLICT | 150 | | P -> A (IN REF. 3 AND 4). |
| FT | CONFLICT | 165 | | S -> P (IN REF. 3; CAA05631). |
| FT | CONFLICT | 505 | | S -> P (IN REF. 3; CAA05631). |
| SQ | SEQUENCE | 530 AA; | 59152 MW; | 36F269D9FD773DA9 CRC64; |
| Query Match | | | | |
| Best local similarity | | 89.08; | Score 2496; | DB 1; Length 530; |
| Matches 468; Conservative | | 88.34; | Pred. No. 1.7e-190; | |
| | | | Mismatches 35; | Indels 0; Gaps 0; |
| Qy | 1 | MDIKNSPSSLSNPNVLP | TPGHLSPVNHQSLHYAEPKSPWCCEARSLEHTLPVN | 120 |
| Db | 1 | MEIKNSPSSLSNPNVLP | TPGHLSPVNHQSLHYAEPKSPWCCEARSLEHTLPVN | 120 |
| Qy | 61 | NTNLEGGPQRTSPNVLP | TPGHLSPVNHQSLHYAEPKSPWCCEARSLEHTLPVN | 120 |
| Db | 61 | STGNLDGPPVRLSPNVLP | TPGHLSPVNHQSLHYAEPKSPWCCEARSLEHTLPVN | 120 |
| Qy | 121 | RETLKRVKSGNRCASPVT | PGSKRDHAFCAVCSYASGYHYGVMSCEGCKAFKRSIQGH | 180 |
| Db | 121 | RETLKRLKSSGSCASPVT | SNAKDAEFCPCVSDYASGYHYGVMSCEGCKAFKRSIQGH | 180 |
| Qy | 181 | NDVICPATNCTIDKNRKSC | QACRLKCYEVGMVXCGSRRCQGVFLVRQSRADQQLH | 240 |
| Db | 181 | NDVICPATNCTIDKNRKSC | QACRLKCYEVGMVXCGSRRCQGVFLVRQSRADQQLH | 240 |
| Qy | 241 | CAGKAKSGGHAPVRELLD | ALSPQVLTLLEAEPHVLISRPSPAPPTTEASMMSLTK | 300 |
| Db | 241 | CLSKAKNGGHAPVRELLD | ALSPQVLTLLEAEPHVLISRPSPAPPTTEASMMSLTK | 300 |
| Qy | 301 | LADKELVHMTSWAKKIPG | FVELSLFDQVRLLESQWMEVLMMGLMWSRIDHPGKLIIPADL | 360 |
| Db | 301 | LADKELVHMTSWAKKIPG | FVELSLFDQVRLLESQWMEVLMMGLMWSRIDHPGKLIIPADL | 360 |
| Qy | 361 | VLDREKCKVEGILEIFDM | LATTSPRELKLOHKEVLCUKAMILLNSSMYPVLTATODA | 420 |
| Db | 361 | VLDREKCKVEGILEIFDM | LATTSPRELKLOHKEVLCUKAMILLNSSMYPVLTATODA | 420 |
| Qy | 421 | DSSKLAHLNNAVTDALV | WVIKSGISSQSQSMELANLMLLSHVHSHASNKGMHLLNMX | 480 |
| Db | 421 | ESSKLTLLNNAVTDALV | WVIKSGISSQSQSVRLANLMLLSHVHSHASNKGMHLLNMX | 480 |
| Qy | 481 | CKNVVPVYDLLEMLNAH | VLRGCKSSITGSECSPAEDSKSKEGSSQNPQSQ | 530 |
| Db | 481 | CKNVVPVYDLLEMLNAH | VLRGCKSSITGSECSSTEDSKNKESSQNLQSQ | 530 |
| RESULT 4 | | | | |
| ESR2 MOUSE | | | | |
| ID | ESR2 MOUSE | STANDARD; | PRT; | 530 AA. |
| AC | O08537; O35635; O70519; | | | |
| DT | 15-JUL-1999 (Rel. 38, Created) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last sequence update) | | | |
| DT | 28-FEB-2003 (Rel. 41, Last annotation update) | | | |
| DE | Estrogen receptor beta (ER-beta). | | | |
| GN | ESR2 OR NR3A2 OR ESRB. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_taxid=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE OF 46-530 FROM N.A., AND MUTAGENESIS. | | | |
| RC | STRAIN=129/Sv; TISSUE=Ovary; | | | |

RA MEDLINE=97211383; PubMed=9058381;
RA Tremblay G.B., Tremblay A., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Labrie P., Giguere V.,
RT "Cloning, chromosomal localization, and functional analysis of the
RL murine estrogen receptor beta";
RL Mol. Endocrinol. 11:353-365(1997).
RN [2]
RP SEQUENCE OF 46-530 FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Ovary;
RX MEDLINE=97424142; PubMed=9280064;
RA Pettersson K., Grandien K., Kuiper G.G.J.M., Gustafsson J.-A.;
RT "Mouse estrogen receptor beta forms estrogen response element-binding
RL heterodimers with estrogen receptor alpha";
RL Mol. Endocrinol. 11:1486-1496(1997).
RN [3]
RP SEQUENCE OF 1-60 FROM N.A.
RC TISSUE=Ovary;
RA Leygue E., Lu B., Dotzlaw H., Glor C., Watson P.H., Murphy L.C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-60 FROM N.A.
RC STRAIN=C57BL/6J X 129; TISSUE=Ovary;
RA Rosenfeld C.S., Lubahn D.B.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP CARBOHYDRATE-LINKAGE SITE SER-61, AND PHOSPHORYLATION SITE SER-61.
RX MEDLINE=20450734; PubMed=1095228;
RA Cheng X., Cole R.N., Zala J., Hart G.W.;
RT "Alternative O-glycosylation/O-phosphorylation of the murine estrogen
RL receptor beta";
RL Biochemistry 39:11609-11620(2000).
RN [6]
RP ALTERNATIVE SPLICING.
RC TISSUE=Ovary;
RX MEDLINE=98348389; PubMed=9685228;
RA Lu B., Leygue E., Dotzlaw H., Murphy L.J., Murphy L.C., Watson P.H.;
RT "Estrogen receptor-beta mRNA variants in human and murine tissues";
RL Mol. Cell. Endocrinol. 138:199-203(1998).
RN [7]
RP TISSUE SPECIFICITY.
RX MEDLINE=98268825; PubMed=9607809;
RA Rosenfeld C.S., Ganjam V.K., Taylor J.A., Yuan X., Stiehr J.R.,
RA Hardy M.P., Lubahn D.B.;
RT "Transcription and translation of estrogen receptor-beta in the male
RL reproductive tract of estrogen receptor-alpha knock-out and wild-type
RL mice";
RL Endocrinology 139:2982-2987(1998).
RN [8]
RP INTERACTION WITH NCOA3.
RX MEDLINE=97336097; PubMed=9132892;
RA Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K.,
RA Rosenfeld M.G.;
RT "The transcriptional co-activator p/CIP binds CBP and mediates
RL nuclear-receptor function";
RL Nature 387:677-684(1997).
RN [9]
RP INTERACTION WITH NCOA6.
RX MEDLINE=20250907; PubMed=10788465;
RA Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,
RA Reddy J.K.;
RT "Isolation and characterization of peroxisome proliferator-activated
RL receptor (PPAR) interacting protein (PRIP) as a coactivator for
RL PPAR";
RL J. Biol. Chem. 275:13510-13516(2000).
CC -I- FUNCTION: Nuclear hormone receptor. Binds estrogens with an
CC affinity similar to that of ESR1 (ER-alpha), and activates
CC expression of reporter genes containing estrogen response elements
CC (ERE) in an estrogen-dependent manner. May play a role in ovarian
CC follicular growth and maturation.
CC -I- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
CC ESR1. Interacts with NCOA3 and NCOA6 coactivators, leading to a
CC strong increase of transcription of target genes. Also interacts
CC with NCOA5 (By similarity).

GN ESR2 OR NR3A2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Ovarian follicle;
RX MEDLINE=99150196; PubMed=10026117;
RA Rosenfeld C.S., Yuan X., Manikkam M., Calder M.D., Garverick H.A.,
RA Lubahn D.B.;
RT "Cloning, sequencing, and localization of bovine estrogen receptor-
RT beta within the ovarian follicle.";
RL Biol. Reprod. 60:691-697(1999).
RN [2]
RP SEQUENCE OF 4-527 FROM N.A.
RX MEDLINE=99359179; PubMed=10432221;
RA Walther N., Lioutas C., Iillmann G., Ivell R.;
RT "Cloning of bovine estrogen receptor beta (Erbeta): expression of
RT novel deleted isoforms in reproductive tissues.";
RL Mol. Cell. Endocrinol. 152:37-45(1999).
CC -i- FUNCTION: Nuclear hormone receptor. Binds estrogens with an
CC affinity similar to that of ESR1 (ER-alpha), and activates
CC expression of reporter genes containing estrogen response elements
CC (ERE) in an estrogen-dependent manner. May play a role in ovarian
CC follicular growth and maturation.
CC -i- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
CC ESR1. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading
CC to a strong increase of transcription of target genes (By
CC similarity).
CC -i- SUBCELLULAR LOCATION: Nuclear.
CC -i- TISSUE SPECIFICITY: Present in granulosa cells of antral follicles
CC in various stages of follicular growth.
CC -i- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -i- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC
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CC
CC -----
CC EMBL; AF110402; AAD24432.1; -.
CC EMBL; Y18017; CAB53861.1; ALT_INIT.
CC HSSP; P03372; IHQO.
CC GO; GO:0005634; C:nucleus; ISS.
CC GO; GO:00030284; F:estrogen receptor activity; ISS.
CC GO; GO:0004879; F:ligand-dependent nuclear receptor activity; ISS.
CC GO; GO:0048019; F:receptor antagonist activity; ISS.
CC GO; GO:0005496; F:steroid binding; ISS.
CC GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
CC GO; GO:0030308; P:negative regulation of cell growth; ISS.
CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Ster_hrmn_receptor.
CC InterPro; IPR008946; Str_ncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00398; STERHORMONER.
CC PRODOM; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOL1; 1.
CC SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Steroid-binding; Phosphorylation.
CC DOMAIN 1 145 MODULATING.

FT DNA BIND 146 211 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 146 166 C4-TYPE.
FT ZN_FING 182 206 C4-TYPE.
FT DOMAIN 212 527 STEROID-BINDING.
FT MOD_RES 84 84 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 485 485 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 60 60 N -> D (IN REF. 2).
SQ SEQUENCE 527 AA; 59031 MW; 9CEFFEL06F4E4C84 CRC64;
Query Match 87.8%; Score 2463.5; DB 1; Length 527;
Best Local Similarity 87.9%; Pred. No. 6.6e-188;
Matches 466; Conservative 22; Mismatches 39; Indels 3; Gaps 1;
QY 1 MDVKSPSSINSPSSINCSQSLPLEHGSIIYIPSSYVDVSHHEYPAMTFYSPAMVYSIFS 60
DB 1 MDVKSPSSINSPSSINCSQSLPLEHGSIIYIPSSYVDVSHHEYPAMTFYSPAMVYSIFS 60
QY 61 NVTNLEGGPGROTTSFNVLTPTFGHLSPLAVHROQLSHLYABPKSPWCSEARSUEHTLPVN 120
DB 61 ---NSEDGPGRTTTSFNVLTPTFGHLSPLAHCQPSVLYAEPOKSPWRETRSLHTLPVN 117
QY 121 RETLKRKVGSGNCPSPVTGPGKRDHFCACVSDVASGHYGVWSCGCEKAFKKSIOGH 180
DB 118 RETLKRKASGSSCASPATSPSSKRDHFCACVSDVASGHYGVWSCGCEKAFKKSIOGH 177
QY 181 NDYICPATNOCCTIDKNRKSQACRLKCYEVMVKCGSRRCGVLVVRORSADQLH 240
DB 178 NDYICPATNOCCTIDKNRKSQACRLKCYEVMVKCGSRRCGVLVVRORSADQLH 237
QY 241 CAGKAKRSGGHAPRVRELLDLSPEQLVLTLEAPPVHLISRPSPAPTEASMMMLTK 300
DB 238 CLSKTRNGPMPTRVKELLSALSPEQLVLTLEAPPVHLISRPSPAPTEASMMMLTK 297
QY 301 LADKELVEMISNAKIPGVFELSFDVRELLESCEVLMGLMYSIDHPGKLIAPDL 360
DB 298 LADKELVEMISNAKIPGVFELSFDVRELLESCEVLMGLMYSIDHPGKLIAPDL 357
QY 361 VLDRDEGCKVEGILETFDMLLATTSRFRELQKHKEYLCVKAMILNSSMYPLVTATDA 420
DB 358 ILDRDEGCKVEGILETFDMLLATTSRFRELQKHKEYLCVKAMILNSSMYPSATAPQA 417
QY 421 DSSRLAHLLNAVTDALVWVIAKSGISSQOQSMRLANLLMLSHVHASKGHEHLINMK 480
DB 418 DSGRLTHLLNAVTDALVWVIAKSGMSQOQSMRLANLLMLSHVHASKGHEHLINMK 477
QY 481 CKNVVPVYDILLLEMLNAHVLRCCKSITGSECSPAEDSKSKGCSQNPQSQ 530
DB 478 CKNVVPVYDILLLEMLNAHVLRCCKSITGSECSPAEDSKSKGCSQNPQSQ 527
RESULT 6
ESR2_SHEEP STANDARD; PRT; 527 AA.
ID_SHEEP
AC Q9TUJ5; Q9N0T6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Estrogen receptor beta (ER-beta).
GN ESR2 OR NR3A2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORMS BETA AND BETA-1).
RC TISSUE=Ovary;
RX MEDLINE=21313342; PubMed=11420232;
RA Cardenas H., Burke K.A., Bigsby R.M., Pope W.F., Nephew K.P.;
RT "Estrogen receptor beta in the sheep ovary during the estrous cycle
RT and early pregnancy.";
RL Biol. Reprod. 65:128-134(2001).
CC -i- FUNCTION: Nuclear hormone receptor. Binds estrogens with an

CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
 CC a DNA-binding domain and a C-terminal steroid-binding domain.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
 CC subfamily.
 CC -----
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 CC -----
 CC EMBL: AF164957; AAD5381.2; -
 CC EMBL: AF267736; AAK15151.1; -
 CC HSP: P03372; IHQ.
 CC GO: GO:0005634; C:nucleus; ISS.
 CC GO: GO:0030284; F:estrogen receptor activity; ISS.
 CC GO: GO:0004879; F:ligand-dependent nuclear receptor activity; ISS.
 CC GO: GO:0048019; F:receptor antagonist activity; ISS.
 CC GO: GO:0005496; F:steroid binding; ISS.
 CC GO: GO:0030520; P:estrogen receptor signaling pathway; ISS.
 CC GO: GO:0030308; P:negative regulation of cell growth; ISS.
 CC GO: GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
 CC InterPro: IPR000536; Hormone rec lig.
 CC InterPro: IPR001723; Steroid receptor.
 CC InterPro: IPR008946; Str ncl receptor.
 CC InterPro: IPR001628; Znf C4steroid.
 CC Pfam: PF00104; hormone rec; 1.
 CC PRINTS: PF00105; zf-C4; 1.
 CC PRINTS: PR00398; STRDHORMONER.
 CC PRINTS: PR00047; STROIDFINGER.
 CC ProDom: PD000035; Znf C4steroid; 1.
 CC SMART: SM00430; HOL1; 1.
 CC SMART: SM00399; ZNF C4; 1.
 CC PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 CC Zinc-finger; Steroid-binding; Phosphorylation.
 CC DOMAIN 1 145 MODULATING.
 CC DNA BIND 146 211 NUCLEAR RECEPTOR-TYPE.
 CC ZN FING 146 166 C4-TYPE.
 CC ZN FING 182 206 C4-TYPE.
 CC DOMAIN 212 526 STEROID-BINDING (BY SIMILARITY).
 CC MOD RES 84 84 PHOSPHORYLATION (BY SIMILARITY).
 CC MOD RES 484 484 PHOSPHORYLATION (BY SIMILARITY).
 CC CONFLICT 317 317 M -> V (IN REF. 2).
 CC CONFLICT 469 469 T -> M (IN REF. 2).
 CC SEQUENCE 526 AA; 58849 MW; 35C2D2661078BF6 CRC64;
 CC -----
 CC Query Match 86.1%; Score 2415; DB 1; Length 526;
 CC Best Local Similarity 86.2%; Pred. No. 4.7e-184;
 CC Matches 457; Conservative 29; Mismatches 40; Indels 4; Gaps 2;
 CC -----
 CC 1 MDIKNSPSSINSSVNCSSQILPLEHGSIVIPSSVVDGSHHEVPANTEVSPAVNYSIS 60
 CC 1 MDIKNSPSSINSSVNCSSQVLPFLPGIYIPSSVYSCHEVSAMTFSPAVNYSIS 60
 CC 61 NVTNLEGGPGQRTSPNVLWPTPGHLSPLVHRLQSLHLYAEPQKSPWCBSAEIHTLPVN 120
 CC 61 --NVEVPGQRTSPNVLWPTPGHLSPLAHCQPSLLYAEQKSPWCDSRLSHTLPVN 117
 CC 121 RETLKRKVSNCASVTPGSGRDAHFCVCSVDYASGHHYGVSCGKAPKRSIQGH 180
 CC 118 RETLKRKAGSSCASVTPSSKEDAHFCVCSVDYASGHHYGVSCGKAPKRSIQGH 177
 CC 181 NDYICPATNCTIDKNRKSQACRLKCVGVGMVACGRRRCGRLVRRQRASDEQLH 240
 CC 178 NDYICPATNCTIDKNRKSQACRLKCVGVGMVACGRRRCGRLVRRQRASDEQLH 237
 CC 241 CAGKAKRSGGHAFVRELLLDALSPQLVLTLEASPPLVLTSPAPTEASMMMLTX 300
 CC 238 CLSRAKNGDHTTRVRELLLSLSPQLVLTLEASPPLVLTSPAPTEASMMMLTX 297

QY 301 LADKELVHMSWAKKIPGVFVLSLDFQVRLLESQWVLMGLMRSIDHPKLIAPDL 360
 DB 298 LADKELVHMSWAKKIPGVFVLSLDFQVRLLESQWVLMGLMRSIDHPKLIAPDL 357
 QY 361 VLDRGKCVGILFDMMLATTSFRFLKQHKYLCVKAMILLNNSMYPLVATODA 420
 DB 358 VLDRGKCVGILFDMMLATTSFRFLKQHKYLCVKAMILLNNSMYPLVATODA 416
 QY 421 DSSRLAHLNNAVTDALVWVIAKSGISSQSQSMRLANLMLLSHVHSHKGMHLNKK 480
 DB 417 ESSRLKTLNNAVTDALVWVIAKSGISSQSQSVRLANLMLLSHVHSHKGMHLNKK 476
 QY 481 CKNVVPTVLDLLEMLNAHVLRGCKSITGSECSPAEDSKSKEGSPQSQ 530
 DB 477 CKNVVPTVLDLLEMLNAHVLRGCKSITGSECSPAEDSKSKEGSPQSQ 526

 RESULT 8
 ESR2 STUVU STANDARD; PRT; 554 AA.
 AC Q9PVE2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estrogen receptor beta (ER-beta).
 GN ESR2 OR NR3A2.
 OS Sturnus vulgaris (Starling).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Sturnus.
 OX NCBI_TaxID=9172;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99427866; PubMed=10499520;
 RA Bernard D.J., Bentley G.E., Balhazart J., Turek F.W., Ball G.P.;
 RT "Androgen receptor, estrogen receptor alpha, and estrogen receptor
 RT beta show distinct patterns of expression in forebrain song control
 RT nuclei of European starlings.";
 RL Endocrinology 140:4633-4643(1999).
 CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF ER-
 CC ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
 CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
 CC LOCALLY SYNTHESIZED ESTROGENS MAY ACT VIA ER BETA, IN ADDITION TO
 CC ER ALPHA, TO MEDIATE SEASONAL OR DEVELOPMENTAL EFFECTS ON NEARBY
 CC SONG NUCLEI.
 CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 CC ALPHA (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: BRAIN, PITUITARY, SKELETAL MUSCLE, LIVER,
 CC ADRENAL, KIDNEY, TESTIS, AND OVARY.
 CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
 CC a DNA-binding domain and a C-terminal steroid-binding domain.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
 CC subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF113513; AAD56593.1; -
 CC HSP: P03372; IHQ.
 CC GO: GO:0005634; C:nucleus; ISS.
 CC GO: GO:0030284; F:estrogen receptor activity; ISS.
 CC GO: GO:0004879; F:ligand-dependent nuclear receptor activity; ISS.
 CC GO: GO:0048019; F:receptor antagonist activity; ISS.
 CC GO: GO:0005496; F:steroid binding; ISS.
 CC GO: GO:0030520; P:estrogen receptor signaling pathway; ISS.
 CC GO: GO:0030308; P:negative regulation of cell growth; ISS.
 CC GO: GO:0006355; P:regulation of transcription, DNA-dependent; ISS.

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Coturnix.
NCBI_TaxID=93934;
[1]
RP SEQUENCE FROM N.A.
RA Foidart A., Lataye B., Grisar T., Ball G.P., Balthazart J.;
RT "Sequence and neuroanatomical distribution of estrogen receptor beta
in the quail brain.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 141-286 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98430913; PubMed=9760113;
RA Lataye B., Foidart A., Grisar T., Balthazart J.;
RT "Partial cloning and distribution of estrogen receptor beta in the
avian brain.";
CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
ALPHA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: A HIGH EXPRESSION IS SEEN IN THE
TELECEPHALON, DIENCEPHALON, PITUITARY, TESTIS AND KIDNEYS BUT
LITTLE OR NO EXPRESSION IS SEEN IN THE CEREBELLUM, PECTORAL MUSCLE
AND ADRENAL GLAND.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
subfamily.

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EMBL: AF045149; AAC36463.2; --
HSSP: P03372; 1HCQ.
GO: GO:0005634; C:nucleus; ISS.
GO: GO:0030284; P:estrogen receptor activity; ISS.
GO: GO:0004879; P:ligand-dependent nuclear receptor activity; ISS.
GO: GO:0048019; P:receptor antagonist activity; ISS.
GO: GO:0005496; F:steroid binding; ISS.
GO: GO:0030520; P:estrogen receptor signaling pathway; ISS.
GO: GO:0030308; P:negative regulation of cell growth; ISS.
GO: GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
InterPro: IPR000536; Hormone_rec_1lg.
DR InterPro: IPR001723; Steroid_receptor.
DR InterPro: IPR008946; Str_ncl_receptor.
DR InterPro: IPR001628; Znf_C4steroid.
PFam: PF00104; hormone_rec; 1.
PFam: PF00105; zf-C4; 1.
PRINTS: PR00398; STRDHORMONER.
DR PRINTS: PR00047; STROIDFINGER.
DR ProDom: PD000035; Znf_C4steroid; 1.
SMART: SM00430; HOLI; 1.
SMART: SM00399; Znf_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 104 MODULATING.
FT DNA_BIND 105 170 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 105 125 C4-TYPE.
FT ZN_FING 141 165 C4-TYPE.
FT DOMAIN 171 472 STEROID-BINDING.
SQ SEQUENCE 472 AA; 53411 MW; DF7A78F0FDBD18BD CRC64;

Query Match 74.9%; Score 2101; DB 1; Length 554;
Best Local Similarity 74.8%; Pred. No. 4.2e-159;
Matches 397; Conservative 50; Mismatches 89; Indels 4; Gaps 3;
OY 2 DIKSPSLNPSVNSQSITLPHEGSIVIPSYVDHSHEYPAWTFYSPAVNYISP 61
Db 26 EIKSPAGVISPAPPCNQSTLTAEHPVIPSSIMESREYSTAFPCSPAWNYIAS 85
OY 62 VTNEGSGRGRTTPSNVLPTPGHLSPLVHRQLSHLYAEPKSPCEARSLEHTLPVR 121
Db 86 FGDPFAVAARTSPSPGALSAPGHLSPLSLQCSSLVAYEQSKLWCARPMPVP 145
OY 122 ETLKKVSGNCAFPV-TGPSKDADHFACVSQYASGYHYGVSCGCKAFFKRSTIQGH 180
Db 146 ETLKKTNGNDCTSPIANNPGSKDAHFACVSQYASGYHYGVSCGCKAFFKRSTIQGH 205
OY 181 NDYICPATNOCTIDNRKKSQAELRKYEVGMVKCGSRRCGYLVRQRSADEBQLH 240
Db 206 NDYICPATNOCTIDNRKKSQAELRKYEVGMVKCGSRRCGYLVRQRSADEBQLH 265
OY 241 CAGKAKRSGCHAPRVRELLLDALSPQVLVTLLAEPPHVLISRPSAPPTFASMMGLTK 300
Db 266 CLGRARRYSEATRVKEILLTVSPQVLTLAEAPPVHLVSRFSKPPTFASMMGLTK 325
OY 301 LADKLHVMIWAKKIPGFVELSLFDQVRLLESQWMLMGLMWRSIDHPGKLIAPDL 360
Db 326 LADKLHVMIWAKKIPGFVELSLFDQVRLLESQWMLMGLMWRSIDHPGKLIAPDL 385
OY 361 VLDRDEGKCVGEILIFOMLATTSRRRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA 420
Db 386 VLDRDEGKCVGEILIFOMLATTSRRRELKLQHKEYLCVKAMILLNSSMYPL--SAEEP 443
OY 421 DSARKLAHLNAVTALVVVIATKSGISQQQSMRLANILLSHVRASNKGMEHLNMK 480
Db 444 BSNRKHLNLNVTEALVVVIATKSGIPSOQYTTRLANILLSHVRASNKGMEHLNMK 503
OY 481 CKNWVPVYDLLLEMLNAHVLRCCKSSI-TGSECSPAEDSKSGESONPQSQ 530
Db 504 CKNWVPVYDLLLEMLNAHVLRCCKSLATHPEFGLEQMEPCSELKRGEPQ 554

RESULT 9
ESR2_COTJA STANDARD; PRT; 472 AA.
ID ESR2_COTJA
AC O93511;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estrogen receptor beta (ER-beta).
OS ESR2 OR NR3A2.
OC Coturnix coturnix japonica (Japanese quail).
OC Fukarvora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Matches 370; Conservative 39; Mismatches 47; Indels 6; Gaps 3;
QY 46 MTFYSPAVNYSIPSNVNLGGPGGQTTSPNVLPWTPGHLSPVLVHROLSHLYAEPOKS 105
DB 1 MAFCSFAMNNTYINAFSGSASVRSQTSPSLWSAPGHLSPVLTLCQSLSLLYAEPOKS 60
QY 106 PWCEARSLEHTLPVNRRTLKRVSGNRCASPV-TGPGSKRDAHFCVCSDYASGYHYGVW 164
DB 61 PWCEARPLPVLVPSRRTLKRVSGNRCASPV-TGPGSKRDAHFCVCSDYASGYHYGVW 120
QY 165 SIEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVMKGSRRRC 224
DB 121 SIEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVMKGSRRRC 180
QY 225 GYELVRRORSADQLHACAGKAKSGHAPRVRELLDALSPEOLVLTLEAPPVHLISR 284
DB 181 GYELVRRORSADQLHACAGKAKSGHAPRVRELLDALSPEOLVLTLEAPPVHLISR 237
QY 285 PSAPFTEASMMSLTKLADKELVHMSWAKKIPGFVELSLFDQVRLLESCHWVLMGLM 344
DB 238 PSKPFTTEASMMSLTKLADKELVHMSWAKKIPGFVELSLFDQVRLLESCHWVLMGLM 297
QY 345 WRSIDHPGKLIAPDLVLDDEKCKVEGILEIFDMLLATTSRPRELKQKVCVKAMI 404
DB 298 WRSIDHPGKLIAPDLVLDDEKCKVEGILEIFDMLLATTSRPRELKQKVCVKAMI 357
QY 405 LNSSMYPLVTATQDADSSRKLHLNNAVTDALVWVIAKSGISSQQSSMRLANLMLSH 464
DB 358 LNSSMYPLVTATQDADSSRKLHLNNAVTDALVWVIAKSGISSQQSSMRLANLMLSH 415
QY 465 VHRASNGMEHLNLMCKKNVVPYDVLLEMLNAHTLRGQRKS 511
DB 416 VHRASNGMEHLNLMCKKNVVPYDVLLEMLNAHTLRGQRKS 463

Query Match 69.5%; Score 1948.5; DB 1; Length 472;
Best Local Similarity 79.3%; Pred. No. 4, 4e-147;
Matches 371; Conservative 38; Mismatches 52; Indels 7; Gaps 4;
QY 46 MTFYSPAVNYSIPSNVNLGGPGGQTTSPNVLPWTPGHLSPVLVHROLSHLYAEPOKS 105
DB 1 MAFCSFAMNNTYINAFSGSASVRSQTSPSLWSAPGHLSPVLTLCQSLSLLYAEPOKS 60
QY 106 PWCEARSLEHTLPVNRRTLKRVSGNRCASPV-TGPGSKRDAHFCVCSDYASGYHYGVW 164
DB 61 PWCEARPLPVLVPSRRTLKRVSGNRCASPV-TGPGSKRDAHFCVCSDYASGYHYGVW 120
QY 165 SIEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVMKGSRRRC 224
DB 121 SIEGCKAPFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEVMKGSRRRC 180
QY 225 GYELVRRORSADQLHACAGKAKSGHAPRVRELLDALSPEOLVLTLEAPPVHLISR 284
DB 181 GYELVRRORSADQLHACAGKAKSGHAPRVRELLDALSPEOLVLTLEAPPVHLISR 237
QY 285 PSAPFTEASMMSLTKLADKELVHMSWAKKIPGFVELSLFDQVRLLESCHWVLMGLM 344
DB 238 PSKPFTTEASMMSLTKLADKELVHMSWAKKIPGFVELSLFDQVRLLESCHWVLMGLM 297
QY 345 WRSIDHPGKLIAPDLVLDDEKCKVEGILEIFDMLLATTSRPRELKQKVCVKAMI 404
DB 298 WRSIDHPGKLIAPDLVLDDEKCKVEGILEIFDMLLATTSRPRELKQKVCVKAMI 357
QY 405 LNSSMYPLVTATQDADSSRKLHLNNAVTDALVWVIAKSGISSQQSSMRLANLMLSH 464
DB 358 LNSSMYPLVTATQDADSSRKLHLNNAVTDALVWVIAKSGISSQQSSMRLANLMLSH 415
QY 465 VHRASNGMEHLNLMCKKNVVPYDVLLEMLNAHTLRGQRKS 511
DB 416 VHRASNGMEHLNLMCKKNVVPYDVLLEMLNAHTLRGQRKS 463

RESULT 11
ESR2_CHICK
ID ESR2_CHICK STANDARD; PRT; 472 AA.
AC QPRTS; 2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estrogen receptor beta (ER-beta) (cERb).
GN ESR2 OR NR3A2.
OS Gallus gallus (Chicken).
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Testis;
RA Suzuki M., Mizuno S., Nakabayashi O.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
ALPHA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
subfamily.
CC
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CC

OX NCBI_TaxID=7937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94386022; PubMed=8793852;
 RA Todo T., Adachi S., Yamauchi K.;
 RT "Molecular cloning and characterization of Japanese eel estrogen
 receptor cDNA."
 RL Mol. Cell. Endocrinol. 119:37-45(1996).
 CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
 CC ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
 CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
 CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 CC ALPHA.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Liver.
 CC -!- INDUCTION: By 17-beta-estradiol.
 CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
 CC a DNA-binding domain and a C-terminal steroid-binding domain.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
 CC subfamily.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB003356; BAA19851.1; -
 CC HSP; P03372; LHCO.
 CC GO: GO:0005634; C:nucleus; ISS.
 CC GO: GO:0030284; P:estrogen receptor activity; ISS.
 CC GO: GO:0004879; Filigand-dependent nuclear receptor activity; ISS.
 CC GO: GO:0048019; F:receptor antagonist activity; ISS.
 CC GO: GO:0005496; F:steroid binding; ISS.
 CC GO: GO:0030520; P:estrogen receptor signaling pathway; ISS.
 CC GO: GO:0030308; P:negative regulation of cell growth; ISS.
 CC GO: GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
 CC InterPro: IPR001723; Hormone rec lig.
 CC InterPro: IPR001723; Steroid-receptor.
 CC InterPro: IPR008946; Str ncl receptor.
 CC InterPro: IPR001628; Znf C4steroid.
 CC Pfam: PF00104; hormone_rec; 1.
 CC Pfam: PF00105; zf-C4; 1.
 CC PRINTS: PR00398; STERDORMONER.
 CC PRINTS: PR00047; STEROIDFINGER.
 CC ProDom: PD000035; Znf_C4steroid; 1.
 CC SMART: SM00430; HOL1; 1.
 CC SMART: SM00399; Znf_C4; 1.
 CC PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 CC Zinc-finger; Steroid-binding.
 CC DOMAIN 15 170 MODULATING.
 CC DNA_BIND 171 236 NUCLEAR RECEPTOR-TYPE.
 CC ZN_FING 171 191 C4-TYPE.
 CC ZN_FING 207 231 C4-TYPE.
 CC DOMAIN 237 573 STEROID-BINDING.
 CC SEQUENCE 573 AA; 63420 MW; 9C64C1D8D39ED4CC CRC64;
 Query Match 55.2%; Score 1549; DB 1; Length 573;
 Best local Similarity 57.7%; Pred. No. 3e-115;
 Matches 313; Conservativity 62; Mismatches 121; Indels 46; Gaps 10;
 QY 13 PSSYNGSQSILPLEHGSYIPSSYVDSHHEYPAMTFYSPAVMYSPNVTNLEGGP--- 69
 DB 33 PTMYNGALPALSMESHAVCIPISTDSHDYAALTFYSPILSH-----GGPVP 82
 QY 70 ----GQQTSPVNLWT---PCHLSPLVHROLSHLYAPQSPWCPEARSLHTLPVNR 122
 DB 83 ESPAPRQSPSPFLWFAHGHGHVSPALHFOPLVREPAPSPWAEKPLEH-----GQ 137

QY 123 TLKRVSGNRCSAPVTGPGS-----KRDHFAVCSDYASGVHYGVWSCGCKAFPKR 175
 DB 138 AQTSKLAGKRWASSEEGTSVGGCFAGKGDHFCVCHDYASGHYGVWSCGCKAFPKR 197
 QY 176 SIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGMVKCGSRRRRCGYFLVRRORSA 235
 DB 198 SIQGHNGYICPATNQCTIDKNRRKSCQACRLKCYEYGMVKCGSRRRRCGYFLVRRORSA 257
 QY 236 D--BOLHCAKGA---KRSQGHAPREVRLLLDLSPQVLVTLLEAEPPHV-LISRPSAPF 289
 DB 258 HIRELAGTGCGARTQREGVVPQTOEAQSAUTPEOLINRIIEAEPEIYLMKELKKPP 317
 QY 290 TEASMMSLTKLADKELVHMSWAKLIPGFGFVLSLFDQVRLLESCHWMEVLMGLMWSID 349
 DB 318 TEDSMMSLTLADKELVHMSWAKLIPGFGFVLSLFDQVRLLESCHWMEVLMGLMWSID 377
 QY 350 HPGLIIFADPLVLDLRGKCVGELIETFDMLLATTSPRELKLOKHEYLCKVMILLNSS 409
 DB 378 HPGLIIFSPOLKLNDRGSCVGEILETFDMVLAATSRELKLOREBYVCLKAILLNP 437
 QY 410 MYPLVTAT-QDADSSRLAHLNVAITDALVMVIAKSGISSQQSMRLANLMLLSHVRHA 468
 DB 438 LCTTSSNRELEBNKLEWDSVTDLVWTAIKGLTFQOQSARLAHLMLLAHRL 497
 QY 469 SNKGKHEHLNMKQNVVYDYLLEMLNAHVLRCCKSSITGSECSPAEDSKSGSQNPQ 528
 DB 498 SNKGKHEHLNMKQNVVYDYLLEMLNAHVLRCCKSSITGSECSPAEDSKSGSQNPQ 550
 QY 529 SQ 530
 DB 551 SQ 552
 RESULT 12
 EMBL CARAU
 ID EMBL CARAU STANDARD; PRT; 568 AA.
 AC Q9W669;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Estrogen receptor beta-1 (ER-beta-1).
 OS Carassius auratus (Goldfish).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Carassius.
 CC NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=99169117; PubMed=10068500;
 RA Tchoudakova A.V., Pathak S., Callard G.V.;
 RT "Molecular cloning of an estrogen receptor beta subtype from the
 RL Gen. Comp. Endocrinol. 113:388-400(1999).
 CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
 CC ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
 CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
 CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
 CC ALPHA (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
 CC a DNA-binding domain and a C-terminal steroid-binding domain.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
 CC subfamily.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC


```

DR EMBL; AF061269; AAD26921.1; -.
DR HSP; P03372; IERR.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Steroid_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
FT ZINC-FINGER; Steroid-binding.
FT DOMAIN 12 169 MODULATING.
FT DNA_BIND 170 235 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 170 190 C4-TYPE.
FT ZN_FING 206 230 C4-TYPE.
FT DOMAIN 226 568 STEROID-BINDING.
SQ SEQUENCE 568 AA; 63539 MW; 2B678D075DB76F9 CRC64;

Query Match 52.3%; Score 1466; DB 1; Length 568;
Best Local Similarity 56.0%; Pred. No. 1.1e-108;
Matches 290; Conservative 75; Mismatches 127; Indels 26; Gaps 10;

Qy 12 SPSSVNCQSITLPLEHGSIVIPSSVVDSSHHEYPAMTFVSPAVMNYSPSNVNLGGPG- 70
Db 38 SP-TFNSSSPSLPVESHPCIPSPYDGLGHDTFTLPFYSPLLGY----GTSPLSDCPV 92

Qy 71 RQTSPNVLNPTPGHLSPLVVRQLSHLYA-EPOKSPWCARSLEHTLPVNRRTLRKVS 129
Db 93 RQSLPTLFWPPHSHVSSSLALHQQOTRLQPNHPTGGTWAELTPDHGCEENCKPLSKRVA 152

Qy 130 GNRCASPVTPGSGKRDHAHPCAVCSYAGSHYGVWSCGCKAPFKRSIOGHNDVICPATN 189
Db 153 VAETS--TSLRGKADMEHYCAVCSYAGSHYGVWSCGCKAPFKRSIOGHNDVICPATN 210

Qy 190 QCTIDKRRKSCQACRLKCYEVGMVKGSGRRRCGYRLVRRQSADEQ--LHCAGKAXR 247
Db 211 QCTIDKRRKSCQACRLKCYEVGMVKGSGRRRCGYRLVRRQSADEQ--LHCAGKAXR 266

Qy 248 SGHAPVR-----ELLDDALSPQLVLTLEAPPV-LISPSAPFTASMMMS 297
Db 267 SGPRSQEIKTVQRPISGNKVVMTALSPBELIARINDABPPPIYLMKDYK3FTEANYMS 326

Qy 298 LTKLADKELVEMISWAKKIPGVFELSLFDQVRLLESQWMEVLMGLMWSIDHPGLIFA 357
Db 327 LTNLADKELVEMISWAKKIPGVFELSLFDQVRLLESQWMEVLMGLMWSVNHFGKLVFS 386

Qy 358 PDLVLDREGKCVGEILEIFDMLLATTSRFRELKLOHKEYLCVKAMILLNSM-YPLVTA 416
Db 387 PDLVLSRDEGSCVQGFABIFDMLLAATSRFRELKLOREYACLKAMILLNSMCLSSAEG 446

Qy 417 TQDADSSPKLAHLNATVDALVWYTAKSIGSSQQSQSMELANLLMLSHVRHASKNGMEHL 476
Db 447 GEELQSRSKLCLLDVSDVALVWYTAKSIGSSQQSQSMELANLLMLSHVRHASKNGMEHL 506

Qy 477 LNAKCKNVPVYDILLENLNAHVLRGCKSSITGSECS 514
Db 507 HSMKWKQVPLVDLLEMLDAHIMGSRLSHSGQADP 544

RESULT 13
ESR2 ONCMY
ID ESR2 ONCMY STANDARD; PRT; 568 AA.
AC P57782;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estrogen receptor beta (ER-beta).
GN ESR2 OR NR3A2.

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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Haug M., Ackermann G., Pent K.;
RT "Molecular cloning of an estrogen receptor beta subtype from rainbow
RT trout.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
CC ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
CC ALPHA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ289883; CAC06714.1; -.
CC HSP; P03372; IERR.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Steroid_receptor.
CC InterPro; IPR008946; Str_ncl_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00398; STRDHORMONER.
CC PRINTS; PR00047; STROIDFINGER.
CC ProDom; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOLI; 1.
CC SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 177 MODULATING.
FT DNA_BIND 178 243 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 178 198 C4-TYPE.
FT ZN_FING 214 238 C4-TYPE.
FT DOMAIN 244 568 STEROID-BINDING.
SQ SEQUENCE 568 AA; 63813 MW; F7A7BD7B3B2C2804 CRC64;

Query Match 51.4%; Score 1440.5; DB 1; Length 568;
Best Local Similarity 54.9%; Pred. No. 1.2e-106;
Matches 289; Conservative 85; Mismatches 121; Indels 31; Gaps 11;

Qy 16 YNCQSITLPLEHGSIVIPSSVVDSSHHEYPAMTFVSPAVMNY-SIPSNVNLGGPGRQTT 74
Db 49 FNSSSPSLPVESHPCIPSPYDGLGHDTFTLPFYSPALLGYGTSPLS----ECSVQSL 104

Qy 75 SPNVLNPTPGHLSPLVVRQLSHLYA-EPOKSPWCARSLEHTLPVNRRTLRKVSNGRC 133
Db 105 SPTLFWPPHSHVSSSLALHQQOTRLQPNHPTGGTWAELTPDHGCEENCKPLSKRVADEE 164

Qy 134 ASPVTGPGSKRDHAHPCAVCSYAGSHYGVWSCGCKAPFKRSIOGHNDVICPATNCTI 193
Db 165 TS--TSLRGKADMEHYCAVCSYAGSHYGVWSCGCKAPFKRSIOGHNDVICPATNCTI 222

Qy 194 DKNRKSCQACRLKCYEVGMVKGSGRRRCGYRLVRRQSADEQ--LHCAGKAKRSGGH 251
Db 223 DKNRKSCQACRLKCYEVGMVKGSGRRRCGYRLVRRQSADEQ--LHCAGKAKRSGGH 278

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QY 252 APRVR-----ELLDAVSPEQVLTLEAEPPHV-LISRPSAPFTEASMMVSLTKL 301
DB 279 SOBKMSVCPCLSGNEVWVNMALTPPELIARIIMDAEPPEIYLMKDMKKPTEANVMSLTNL 338
QY 302 ADKELVHMSWAKKIPGVFVLSLPDQVLLSCWMEVLMGLMWSIDHPCKLIFAPDLV 361
DB 339 ADKELVHMSWAKKIPGVFVLSLPDQVLLSCWMEVLMGLMWSVNHPPKLIFFSPDLS 398
QY 362 LDRDGKCVGEGILEIFDMLLATTFRFELKQHKYLCVKAMILNNSMYPVLTATODAD 421
DB 399 LSRDGSVCQGVFEIFDMLLAATFRFELKQREYVCLKAMILNNSM--CLSSSGEGE 456
QY 422 SSR---KLHLLNATVLDALVWIAKSGJSSQOQNRLANLMLSHVHRASNKGVHLLN 478
DB 457 ELQRSKLLDSDVTDALVWIAKSGJSSQOQNRLANLMLSHVHRASNKGVHLLN 516
QY 479 MKCNVVPVYDILLENLAHVLARGCKSSITGSECSAPEDSKSKGS 524
DB 517 MKCKQWVLYDILLENLAHVLARGCKSSITGSECSAPEDSKSKGS 560

RESULT 14
ESR2 MICUN STANDARD; PRT; 673 AA.
ID ESR2 MICUN
AC P57781;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Estrogen receptor beta (ER-beta).
ESR2 OR NR3A2.
OS Micropogonias undulatus (Atlantic croaker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sciaenidae; Micropogonias.
OX NCBI_taxID=29154;
RN SEQUENCE FROM N.A.
RX MEDLINE=20461442; PubMed=11005855;
RA Hawkins M.B., Thornton J.W., Crews D., Skipper J.K., Dotte A.,
RT "Identification of a third distinct estrogen receptor and
RT reclassification of estrogen receptors in teleosts.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10751-10756(2000).
CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
CC ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.
CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
CC ALPHA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: ABUNDANT IN THE LIVER AND TESTES, LESS
CC ABUNDANT IN THE OVARY AND BARELY DETECTABLE IN THE MUSCLE.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.

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-----
EMBL; AF298181; AAC16711.1; -.
RSP; P03372; IHCO.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Steroid_receptor.
InterPro; IPR008946; Str_ncl_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.

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DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PRO0398; STRDHORMONER.
DR PRINTS; PRO0047; STROIDFINGER.
DR ProDom; PD00035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 181 MODULATING.
FT DNA_BIND 182 247 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 182 202 C4-TYPE.
FT ZN_FING 218 242 C4-TYPE.
FT DOMAIN 248 653 STEROID-BINDING.
FT SEQUENCE 673 AA; 74680 MW; 2839451577E3D01 CRC64;

Query Match 51.0%; Score 1431; DB 1; Length 673;
Best Local Similarity 53.5%; Pred. No. 8.5e-106;
Matches 303; Conservative 76; Mismatches 125; Indels 62; Gaps 18;

QY 6 SPSSLNPPSYNCQSITLPLEHSGSIVIPSSVYDSHHEY----PAMTEVSPAVNMYSIPSN 61
DB 31 SPGLL--PAVYS---PPLGMDSHIVCLIPSPYTOSSHEYNHSHGLPTIYFSVLSYRPP- 84
QY 62 VTNLEGGQGR--QVTSFNVLMPTFGH--LSPLVVRHQLSHLYABPQ-KSPWCEAR----- 111
DB 85 ITN---SPSSILCPSLSPSAFWSHNPHTMPSLTLCPEISIVYNPSHPAFWLESKAHSIN 141
QY 112 -SLEHTLPVNRFTLKRKVG-----NRCASPTVPGSKEDAFCAVCSYASGYHYGVW 164
DB 142 ASSSSIGCNKSLVYKRSSEGVNDSLSASV-----GKADMFCAVCHDYASYHYGVW 197
QY 165 SCGCKAFFKRSIQGHNDYICPATNOCTIDNRRKSCQACRLRKYEVGMVVKCSRRERC 224
DB 198 SCGCKAFFKRSIQGHNDYICPATNOCTIDNRRKSCQACRLRKYEVGMVVKCSRRERC 257
QY 225 GYRLVRRQRS-----ADEQLHCAGKAKRSGH-----AP--RYRELLLDALSP 265
DB 258 SYRGARHRRGGLQPRDPTGRGLVRVGLGSAQSHLHLEAPLTPLAPTLQAKHVLWSMP 317
QY 266 EQLVLTLEAEPPHV-LISRPSAPFTEASMMVSLTKLADKELVHMSWAKKIPGVFVLSL 324
DB 318 EEFISRIIMDAEPPEIYLMEDLKKEPTEASMMVSLTKLADKELVHMSWAKKIPGVFVLSL 377
QY 325 FDOVRLLESQWMEVLMGLMWSIDHPCKLIFAPDLVLDRECKGVGILFIDMLLATT 384
DB 378 ADGINLKKCCWLETLMLGLMWSVDHPGKLIFFSPDFKLNREEGQCVGEGIMEIPDMLLAGT 437
QY 385 SRREELKQHKYLCVKAMILNNSMYPVLTAT-QQADSSRKLHLNATVLDALVWIAK 443
DB 438 SRREELKQHKYLCVKAMILNNSMYPVLTAT-QQADSSRKLHLNATVLDALVWIAK 497
QY 444 SGISSQQOQNRLANLMLSHVHRASNKGVHLLNKKVVPVYDILLENLAHVLARGC 503
DB 498 MGLTQQOQNRLANLMLSHVHRASNKGVHLLNKKVVPVYDILLENLAHVLARGC 556
QY 504 KSITGSECSAPEDSKS-KESQNPQ 528
DB 557 -----GSPSSPSSETYSQHQYTPQ 577

RESULT 15
ESR2 MACMU STANDARD; PRT; 279 AA.
ID ESR2 MACMU
AC Q9TTE5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Estrogen receptor beta (ER-beta) (Fragment).
ESR2 OR NR3A2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Rutheria; Primates; Catarrhini; Cercopithecoidea;

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OC Cercopithecinae; Macaca.
OX NCBI_taxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20113291; PubMed=10644527;
RA Wu X.H., Ma X.H., Smith G.C.S., Nathanielsz P.W.;
RF "Differential distribution of ERalpha and ERbeta mRNA in intrauterine
RL tissues of the pregnant rhesus monkey.";
RL Am. J. Physiol. 278:C190-C198(2000).
CC -!- FUNCTION: Nuclear hormone receptor. Binds estrogens with an
CC affinity similar to that of ESR1 (ER-alpha), and activates
CC expression of reporter genes containing estrogen response elements
CC (ERE) in an estrogen-dependent manner. May play a role in ovarian
CC follicular growth and maturation.
CC -!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
CC ESR1. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading
CC to a strong increase of transcription of target genes (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF119229; AAD54069.1; --
CC HSSP: P03372; 1ERR.
CC InterPro: IPR000536; Hormone_rec_lig.
CC InterPro: IPR001723; Steroid_receptor.
CC InterPro: IPR008946; Str_ncl_receptor.
CC InterPro: IPR001628; Znf_C4steroid.
CC Pfam: PF00104; hormone_rec; 1.
CC PRINTS: PR00398; STRDHORMONER.
CC SMART: SM00430; HOL1; 1.
CC PROSITE: PS00031; NUCLEAR RECEPTOR; PARTIAL.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Steroid-binding; Phosphorylation.
CC NON_TER 1
CC DOMAIN <1 >279 STEROID-BINDING.
CC MOD_RES 251 251 PHOSPHORYLATION (BY SIMILARITY).
CC NON_TER 279 279
CC SEQUENCE 279 AA; 858D9B7D01DA0301 CRC64;
CC -----
Query Match 49.8%; Score 1398; DB 1; Length 279;
Best Local Similarity 98.2%; Pred. No. 1.1e-103;
Matches 274; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 238 QLEHCAGKAKRSQGHAPVRELLLDALSPQLVLTLEAAPPVHLISRPSPAPTEASMMMS 297
Db 1 QLEHCAGKAKRSQGHAPVRELLLDALSPQLVLTLEAAPPVHLISRPSPAPTEASMMMS 60
QY 298 LTKLADKELVHMSWAKKIPGFVVELSLFDQVRLLESQWNEVLMVGLMWSIDHPGKLIIPA 357
Db 61 LTKLADKELVHMSWAKKIPGFVVELSLFDQVRLLESQWNEVLMVGLMWSIDHPGKLIIPA 120
QY 358 PDLVLDRDGKCVGEGILEIFDMLATTSRFREKLQHKYLCVKAMILLNSMYPLVTAT 417
Db PDLVLDRDGKCVGEGILEIFDMLATTSRFREKLQHKYLCVKAMILLNSMYPLVTAT 180
QY 418 QDADSSRKLHLINAVTDALVWVIAXSGISSQQSQMRLANLLMLLSHVHASNKGMEHLL 477
Db 181 QDADSSRKLHLINAVTDALVWVIAXSGISSQQSQMRLANLLMLLSHVHASNKGMEHLL 240
QY 478 NMKCKKVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAE 516
Db 241 SMKCKKVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAE 279
```

Search completed: June 20, 2004, 10:37:40
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: June 20, 2004, 10:34:32 ; Search time 46 Seconds
(without alignments)
3635.318 Million cell updates/sec

Title: US-08-906-365-2

Perfect score: 2805
Sequence: 1 MDKNSPSSLSNPPSYNCSQ.....ECSPABDSKSKGQNPQSQ 530

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------|
| 1 | 2483 | 88.5 | 567 | 11 | Q8BG65 mus musculus |
| 2 | 2420 | 86.3 | 499 | 6 | Q5MFO macaca arct |
| 3 | 2317 | 82.6 | 486 | 6 | Q5ME99 callithrix |
| 4 | 2273 | 81.0 | 503 | 11 | Q91286 mus musculus |
| 5 | 1723 | 61.4 | 323 | 4 | Q86231 homo sapien |
| 6 | 1691 | 60.3 | 542 | 13 | Q902E6 |
| 7 | 1553 | 55.4 | 335 | 11 | Q8CGK9 |
| 8 | 1471.5 | 52.5 | 559 | 13 | Q8JUB9 |
| 9 | 1455.5 | 51.9 | 553 | 13 | Q7ZU32 |
| 10 | 1454.5 | 51.9 | 553 | 13 | Q90WS8 |
| 11 | 1441.5 | 51.4 | 553 | 13 | Q8AV62 |
| 12 | 1410.5 | 50.3 | 565 | 13 | Q8QHK9 |
| 13 | 1409.5 | 50.2 | 553 | 13 | Q8OQK7 |
| 14 | 1401 | 49.9 | 671 | 13 | Q7TK27 |
| 15 | 1397.5 | 49.8 | 592 | 13 | Q90WS9 brachydanio |
| 16 | 1396 | 49.8 | 601 | 13 | Q7T3U5 candidia ba |

| | | | | | |
|----|--------|------|-----|----|--------------------|
| 17 | 1389.5 | 49.5 | 553 | 13 | Q98SM7 |
| 18 | 1389.5 | 49.5 | 592 | 13 | Q98SM8 |
| 19 | 1388.5 | 49.5 | 612 | 13 | Q7T3U4 varicorhinu |
| 20 | 1366 | 48.7 | 562 | 13 | Q8UW75 oryzias lat |
| 21 | 1293 | 44.3 | 250 | 6 | Q95JC0 canis famil |
| 22 | 1235.5 | 44.0 | 581 | 13 | Q8UWA9 |
| 23 | 1232.5 | 43.9 | 589 | 13 | Q8AYH0 |
| 24 | 1216.5 | 43.4 | 587 | 13 | Q8UWB0 |
| 25 | 1213 | 43.2 | 570 | 13 | Q8OQ02 |
| 26 | 1199 | 42.7 | 574 | 13 | Q7T2K8 |
| 27 | 1188 | 42.4 | 564 | 13 | Q90WV1 |
| 28 | 1180.5 | 42.1 | 620 | 13 | Q7SZ10 |
| 29 | 1172.5 | 41.8 | 583 | 13 | Q8O4Q6 |
| 30 | 1166.5 | 41.6 | 578 | 13 | Q8QHL0 |
| 31 | 1165.5 | 41.6 | 431 | 6 | Q95L13 |
| 32 | 1157 | 41.2 | 620 | 13 | Q90WH6 |
| 33 | 1118 | 39.9 | 554 | 13 | Q90ZM8 |
| 34 | 1099 | 39.2 | 458 | 13 | Q9DDJ3 |
| 35 | 942.5 | 33.6 | 335 | 13 | Q9DDZ4 |
| 36 | 900 | 32.1 | 208 | 11 | Q8K4S0 |
| 37 | 831.5 | 29.6 | 353 | 11 | Q8CGK8 |
| 38 | 679 | 24.2 | 276 | 13 | Q91984 |
| 39 | 659 | 23.5 | 134 | 6 | Q864V2 |
| 40 | 643 | 22.9 | 466 | 11 | Q8CHC9 |
| 41 | 622.5 | 22.2 | 433 | 11 | Q8C7A6 |
| 42 | 622.5 | 22.2 | 434 | 11 | Q8OV81 |
| 43 | 615.5 | 21.9 | 433 | 11 | Q8CCV5 |
| 44 | 594.5 | 21.2 | 200 | 13 | Q90Z59 |
| 45 | 544 | 19.4 | 139 | 11 | Q9JMW7 |

ALIGNMENTS

RESULT 1

Q8BG65 PRELIMINARY; PRT; 567 AA.

AC Q8BG65; 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Estrogen receptor 2.
GN ESR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK054290; BAC35770.1; -
DR EMBL; AK054413; BAC35770.1; -
DR PIR; PT0649; PT0712.
DR MGD; MGI:105392; Esr2.
DR GO; GO:0005496; P:steroid binding; IDA.
DR GO; GO:0007420; P:brain development; IMP.
DR GO; GO:0006928; P:cell motility; IMP.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.
DR InterPro; IPR000536; Hormone rec lig.
DR InterPro; IPR001723; Sterhmrn receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMNER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.

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DR SMART; SMO0430; HOLI; 1.
DR SMART; SMO0399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
SQ SEQUENCE 567 AA; 63217 MW; BFB388C189FABE78 CRC64;

Query Match      88.5%; Score 2483; DB 11; Length 567;
Best Local Similarity 85.8%; Pred. No. 3.4e-219; Indels 18; Gaps 1;
Matches 470; Conservative 25; Mismatches 35;

QY 1 MDIKNSPSSLSNPSYNCOSILPLEHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNYSPS 60
DB 20 MEIKNSPSSLSNPSYNCOSILPLEHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNYSPS 79
QY 61 NVTNLEGGPGROTPSPNVLMWTFPGHLSPLVHROLSHLYAPQKSPWCEARSLEHTLPVN 120
DB 80 STGNLEGGPGROTPSPNVLMWTFPGHLSPLVHROLSHLYAPQKSPWCEARSLEHTLPVN 139
QY 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSYASGYHYGVWSCGCKAFAFKRSIQGH 180
DB 140 RETLKRKLGSGCASPVTPSPAKRDHAFCAVCSYASGYHYGVWSCGCKAFAFKRSIQGH 199
QY 181 NDYICPATNQCTIDKNRKSCQACRLKCYEVGMVKGSRERCGYLRVRRQSADEQLH 240
DB 200 NDYICPATNQCTIDKNRKSCQACRLKCYEVGMVKGSRERCGYLRVRRQSADEQLH 259
QY 241 CAGKAKRSGGHAPRVRELLLDALSPQQLVLTLLAEPPHVLISRPSAPFTEASMMMSLTK 300
DB 260 CLNKAARTSGHTPRVXKELLANSLSPEQLVLTLLAEPPHVLISRPSAPFTEASMMMSLTK 319
QY 301 LADKELVHMI SWAKKIPGFVLSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLI FAPDL 360
DB 320 LADKELVHMI SWAKKIPGFVLSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLI FAPDL 379
QY 361 VLD-----RDEGKCVGEILEIFDMLLATTSRFRKLQHKVEYLCVKA 402
DB 380 VLDSSSDPHHVAQTSKAVPRDEGKCVGEILEIFDMLLATTSRFRKLQHKVEYLCVKA 439
QY 403 MILLNSMYPLVTATQDADSRKLAHLNVAITDALVWVIAKSGISSQQSRLANLMLL 462
DB 440 MILLNSMYPLATASQEAESRKLTHLLNVAITDALVWVIAKSGISSQQSRLANLMLL 499
QY 463 SHVRHASKNGMEHLNKKVVPVYDILLMLNAHLVLRGCKSSITSGECPAEDSKSKE 522
DB 500 SHVRHASKNGMEHLNKKVVPVYDILLMLNAHLVLRGCKSSITSGECPAEDSKSKE 559
QY 523 GSQNPQSQ 530
DB 560 GSQNLQSQ 567

RESULT 2
Q95MF0 PRELIMINARY; PRT; 499 AA.
AC Q95MF0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Estrogen receptor beta 2.
GN ERBETA2.
OS Macaca arctoides (Stump-tailed macaque).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9540;
RN [1]
RP SEQUENCE FROM N.A.
RA Scobie G.A., Wilson J.A., Millar M.R., Macpherson S., Saunders P.T.;
RT "The estrogen receptor beta variant ERBETA cx/ERBETA2 is expressed in
RT a wide range of tissues in both Old and New World primates.";
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AF393815; AAK71317.1; -.
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DR GO; GO:0005634; C:nucleus; ISS.
DR GO; GO:0002844; F:estrogen receptor activity; ISS.
DR GO; GO:0048019; F:receptor antagonist activity; ISS.
DR GO; GO:0005496; F:steroid binding; ISS.
DR GO; GO:0030520; P:estrogen receptor signaling pathway; ISS.
DR GO; GO:0030308; P:negative regulation of cell growth; ISS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
DR InterPro; IPR000516; Hormone rec lig.
DR InterPro; IPR001723; Steroid_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STERDORMONER.
DR PROSITE; PRO0047; STROIDDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SMO0430; HOLI; 1.
DR SMART; SMO0399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 499 AA; 55782 MW; A91DA345C8718COA CRC64;

Query Match      86.3%; Score 2420; DB 6; Length 499;
Best Local Similarity 95.6%; Pred. No. 1.7e-213; Indels 0; Gaps 0;
Matches 456; Conservative 6; Mismatches 15;

QY 1 MDIKNSPSSLSNPSYNCOSILPLEHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNYSPS 60
DB 1 MDIKNSPSSLSNPSYNCOSILPLEHSGSIYIPSSYVDSSHHEYPAMTFYSPAVMNYSPS 60
QY 61 NVTNLEGGPGROTPSPNVLMWTFPGHLSPLVHROLSHLYAPQKSPWCEARSLEHTLPVN 120
DB 61 NVTNLEGGPGROTPSPNVLMWTFPGHLSPLVHROLSHLYAPQKSPWCEARSLEHTLPVN 120
QY 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSYASGYHYGVWSCGCKAFAFKRSIQGH 180
DB 121 RETLKRKVSNGRCASPVTPSPSKRDHAFCAVCSYASGYHYGVWSCGCKAFAFKRSIQGH 180
QY 181 NDYICPATNQCTIDKNRKSCQACRLKCYEVGMVKGSRERCGYLRVRRQSADEQLH 240
DB 181 NDYICPATNQCTIDKNRKSCQACRLKCYEVGMVKGSRERCGYLRVRRQSADEQLH 240
QY 241 CAGKAKRSGGHAPRVRELLLDALSPQQLVLTLLAEPPHVLISRPSAPFTEASMMMSLTK 300
DB 241 CAGKAKRSGGHTPLVRELLLDALSPQQLVLTLLAEPPHVLISRPSAPFTEASMMMSLTK 300
QY 301 LADKELVHMI SWAKKIPGFVLSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLI FAPDL 360
DB 301 LADKELVHMI SWAKKIPGFVLSLFDQVRLLESQWMEVLMGLMWRSIDHPGKLI FAPDL 360
QY 361 VLDREDEKCVGEILEIFDMLLATTSRFRKLQHKVEYLCVKA MILLNSMYPLVTATQDA 420
DB 361 VLDREDEKCVGEILEIFDMLLATTSRFRKLQHKVEYLCVKA MILLNSMYPLVTATQDA 420
QY 421 DSSRKLHLNVAITDALVWVIAKSGISSQQSRLANLMLLSHVRHASKNGMEHL 477
DB 421 DSSRKLHLNVAITDALVWVIAKSGISSQQSRLANLMLLSHVRHASKNGMEHL 477

RESULT 3
Q95ME9 PRELIMINARY; PRT; 486 AA.
AC Q95ME9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Estrogen receptor beta 2.
GN ERBETA2.
OS Callithrix jacchus (Common marmoset).
OC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
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| | | | |
|-----------------------|---|-----------------------|---|
| DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) | DT | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) |
| DE | Estrogen receptor beta type II splice variant. | DE | Estrogen receptor beta type II splice variant. |
| GN | ESR2. | GN | ESR2. |
| OS | Mus musculus (Mouse). | OS | Mus musculus (Mouse). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| OX | NCBI_TaxID=10090; | OX | NCBI_TaxID=10090; |
| RN | [1] | RN | [1] |
| RP | SEQUENCE FROM N.A. | RP | SEQUENCE FROM N.A. |
| RC | STRAINE-DDI; | RC | STRAINE-DDI; |
| RA | Dang Z., van Besooijen R., Karperien M., Papapoulos S., Lowik C.; | RA | Dang Z., van Besooijen R., Karperien M., Papapoulos S., Lowik C.; |
| RT | "Exposure of KS483 cells to estrogen enhances osteogenesis and | RT | "Exposure of KS483 cells to estrogen enhances osteogenesis and |
| RT | inhibits adipogenesis."; | RT | inhibits adipogenesis."; |
| RL | J. Bone Miner. Res. 0:0-0(2001). | RL | J. Bone Miner. Res. 0:0-0(2001). |
| CC | -/- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY. | CC | -/- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY. |
| CC | -/- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). | CC | -/- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). |
| DR | EMBL; AY054413; AAL15175.1; -. | DR | EMBL; AY054413; AAL15175.1; -. |
| DR | MGI; 109392; ESR2. | DR | MGI; 109392; ESR2. |
| DR | GO; GO:0005496; F:steroid binding; IDA. | DR | GO; GO:0005496; F:steroid binding; IDA. |
| DR | GO; GO:0007420; P:brain development; IMP. | DR | GO; GO:0007420; P:brain development; IMP. |
| DR | GO; GO:0006928; P:cell motility; IMP. | DR | GO; GO:0006928; P:cell motility; IMP. |
| DR | GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA. | DR | GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA. |
| DR | InterPro; IPR000536; Hormone_rec_lig. | DR | InterPro; IPR000536; Hormone_rec_lig. |
| DR | InterPro; IPR001723; Stdrhm_receptor. | DR | InterPro; IPR001723; Stdrhm_receptor. |
| DR | InterPro; IPR008946; Str_ncl_receptor. | DR | InterPro; IPR008946; Str_ncl_receptor. |
| DR | InterPro; IPR001628; Znf_C4steroid. | DR | InterPro; IPR001628; Znf_C4steroid. |
| DR | Pfam; PF00104; hormone_rec; 1. | DR | Pfam; PF00104; hormone_rec; 1. |
| DR | Pfam; PF00105; zf_C4; 1. | DR | Pfam; PF00105; zf_C4; 1. |
| DR | PRINTS; PR00398; STRDHORMONER. | DR | PRINTS; PR00398; STRDHORMONER. |
| DR | PRINTS; PR00047; STROIDFINGER. | DR | PRINTS; PR00047; STROIDFINGER. |
| DR | ProDom; PD000035; Znf_C4steroid; 1. | DR | ProDom; PD000035; Znf_C4steroid; 1. |
| DR | SMART; SM00430; HOL1; 1. | DR | SMART; SM00430; HOL1; 1. |
| DR | SMART; SM00399; ZNF C4; 1. | DR | SMART; SM00399; ZNF C4; 1. |
| DR | PROSITE; PS00031; NUCLEAR RECEPTOR; 1. | DR | PROSITE; PS00031; NUCLEAR RECEPTOR; 1. |
| DR | DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription; | DR | DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription; |
| KW | Transcription regulation; Zinc; Zinc-finger. | KW | Transcription regulation; Zinc; Zinc-finger. |
| KW | Transcription regulation; Zinc; Zinc-finger. | KW | Transcription regulation; Zinc; Zinc-finger. |
| SQ | SEQUENCE 486 AA; 54344 MW; 4B29385B7371F277 CRC64; | SQ | SEQUENCE 486 AA; 54344 MW; 4B29385B7371F277 CRC64; |
| Query Match | 82.6%; Score 2317; DB 6; Length 486; | Query Match | 81.0%; Score 2273; DB 11; Length 503; |
| Best Local Similarity | 91.0%; Pred. No. 4.9e-204; | Best Local Similarity | 85.7%; Pred. No. 5.7e-200; |
| Matches | 434; Conservative 18; Mismatches 25; Indels 0; Gaps 0; | Matches | 431; Conservative 22; Mismatches 32; Indels 18; Gaps 1; |
| QY | 1 MDIKRSPSLNPSPPSYNCQSITLPLEHCSIYIPSSYVDSSHHEYPAMFYSPANNVYIPS 60 | QY | 46 MTFYSPAVMNTSIPSNVNTLGGGPGRQITSPNVLWPTPGHLSPLVVRQSLHYAEPQKS 105 |
| DB | 1 MDIKRSPSLNPSPPSYNFGQSITLPLEHGPITYIPSSYVESHEYPAMFYSPANNVYIPS 60 | DB | 1 MTFYSPAVMNTSVSPSTGNLEGGPVQRTASPNVLWFTSGHLSPLATHCQSSLLYAEPOKS 60 |
| QY | 61 MVTNLEGGPGRQITSPNVLWPTPGHLSPLVVRQSLHYAEPQKSPWCEARSLEHTLPVN 120 | QY | 106 PWCEARSLEHTLPVNRRETLKRVKSGNRCASPVTPGSKRDAHFCAVCSVDYASGHHYGVWS 165 |
| DB | 61 SVTNLEGGPGRQITSPNVLWPTPGHLSPLVVRQSLHYAEPQKSPWCEARSLEHTLPVS 120 | DB | 61 PWCEARSLEHTLPVNRRETLKRVKSGSGCASPVTPSKAKRDAHFCAVCSVDYASGHHYGVWS 120 |
| QY | 121 RETLKKVSGNRCASPVTPGSKRDAHFCAVCSVDYASGHHYGVWSCEGCKAFKRSIQGH 180 | QY | 166 CEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQACRLKCYEVMGKCGRRRCRG 225 |
| DB | 121 RETLKKVSGNRCASPVTPGSKRDAHFCAVCSVDYASGHHYGVWSCEGCKAFKRSIQGH 180 | DB | 121 CEGCKAFKRSIQGHNDYICPATNQCTIDKRRKSCQACRLKCYEVMGKCGRRRCRG 180 |
| QY | 181 NDYICPATNQCTIDKRRKSCQACRLKCYEVMGKCGRRRCRGYRLVRQRASDQLH 240 | QY | 226 YRLVRQRASDQLHFCAGKAKRSQGHAPVRRELLDALSPEQLVLTLEAEPHVLISRP 285 |
| DB | 181 NDYICPATNQCTIDKRRKSCQACRLKCYEVMGKCGRRRCRGYRLVRQRASDQLH 240 | DB | 181 YRIVRQRASDQLHFCAGKAKRSQGHAPVRRELLDALSPEQLVLTLEAEPHVLISRP 240 |
| QY | 241 CAGKAKRSQGHAPVRRELLDALSPEQLVLTLEAEPHVLISRPSPAPPTASMMNSLTK 300 | QY | 286 SAPPTASMMNSLTKLADKELVHMLSWAKKIPGFVELSLFQVRLLESCHWVLMGLMW 345 |
| DB | 241 CAGKAKRSQGHAPVRRELLDALSPEQLVLTLEAEPHVLISRPSPAPPTASMMNSLTK 300 | DB | 241 SMPPTASMMNSLTKLADKELVHMLGWAKKIPGFVELSLDQVRLLESCHWVLMGLMW 300 |
| QY | 301 LADKELVHMLSWAKKIPGFVELSLDQVRLLESCHWVLMGLMWRSIDHFGKLIAPDL 360 | QY | 346 RSIDHFGKLIAPDLVLD-----RDGKCVGILIFPMKLIATTSRP 387 |
| DB | 301 LADKELVHMLSWAKKIPGFVELSLDQVRLLESCHWVLMGLMWRSIDHFGKLIAPDL 360 | DB | 301 RSIDHFGKLIAPDLVLD-----RDGKCVGILIFPMKLIATTSRP 360 |
| QY | 361 VLDRDEGKCVGILEIFDMLLATTSSRFRELKLOHKEYLCVKAMILLNSMYPVLTATQDA 420 | QY | 388 RELKLOHKEYLCVKAMILLNSMYPVLTATQDASSRLKHLNNAVTDALVWVIAKSGIS 447 |
| DB | 361 VLDRDEGKCVGILEIFDMLLATTSSRFRELKLOHKEYLCVKAMILLNSMYPVLTATQDA 420 | DB | 361 RELKLOHKEYLCVKAMILLNSMYPVLTATQDASSRLKHLNNAVTDALVWVIAKSGIS 420 |
| QY | 421 DSSRLKHLNNAVTDALVWVIAKSGISQSQSQSMRLANMLLSHVHSHASNGKMHLL 477 | QY | 448 SQSQSMRLANMLLSHVHSHASNGKMHLLNKKCNVVPVYDLLLLLEMLNAHVLRCKKSI 507 |
| DB | 421 DSSRLKHLNNAVTDALVWVIAKSGISQSQSQ | | |

RESULT 4

Q91286
ID 0912

AC Q912
DE Q1 - E

DT 01-D

| | | | |
|--|--|---|--------------|
| QY | 508 | TGSECSPAEDSKSKEGSQNPOSQ | 530 |
| DB | 481 | SGSECSTEDSKSKEGSQMLSQ | 503 |
| RESULT 5 | | | |
| ID | Q85Z31 | PRELIMINARY; | PRT; 323 AA. |
| AC | Q86Z31; | | |
| DT | 01-JUN-2003 (TREMBlrel. 24, Created) | | |
| DT | 01-JUN-2003 (TREMBlrel. 24, Last sequence update) | | |
| DT | 01-OCT-2003 (TREMBlrel. 25, Last annotation update) | | |
| DE | Hypothetical 35.9 kDa protein. | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| OX | NCBI_Taxid=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | TISSUE=Testis; | | |
| RA | Strausberg R.; | | |
| RL | Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; BC024181; AAH24181.1; - | | |
| DR | GO; GO:0005634; C:nucleus; IEA. | | |
| DR | GO; GO:0003700; F:transcription factor activity; IEA. | | |
| DR | GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA. | | |
| DR | InterPro; IPR008946; Str ncl receptor. | | |
| DR | InterPro; IPR001628; Znf C4steroid. | | |
| DR | Pfam; PF00105; zf-C4; 1_- | | |
| DR | PRINTS; PR00047; STROIDFINGER. | | |
| DR | ProDom; PD000035; Znf_C4steroid; 1. | | |
| DR | SMART; SM00393; Znf_C4; 1. | | |
| DR | PROSITE; PS00031; NUCLEAR_RECEPTOR; 1. | | |
| KW | Hypothetical protein. | | |
| SQL | SEQUENCE 323 AA; 3594k MW; 158D376C56D3CA12 CRC64; | | |
| Query Match 61.4%; Score 1723; DB 4; Length 323; | | | |
| Best Local Similarity 100.0%; Pred. No. 1.le-149; | | | |
| Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| QY | 1 | MDIKNSPSLSNPSSYNCSQILPLEHGSIYIPSYVDSHHYPAMTFYSPAVMYNISPS | 60 |
| DB | 1 | MDIKNSPSLSNPSSYNCSQILPLEHGSIYIPSYVDSHHYPAMTFYSPAVMYNISPS | 60 |
| QY | 61 | NVTNLGGGRGRTTSPLVLTPTPGHSLPLVVHROLSHLYAEPOKSPWCPEARSLHTLPVN | 120 |
| DB | 61 | NVTNLGGGRGRTTSPLVLTPTPGHSLPLVVHROLSHLYAEPOKSPWCPEARSLHTLPVN | 120 |
| QY | 121 | RETLKRKYSGNRCAFPVTGPQSKRDHAFCVCSYASGYHYGVWSCCGCKAFPKRSIQGH | 180 |
| DB | 121 | RETLKRKYSGNRCAFPVTGPQSKRDHAFCVCSYASGYHYGVWSCCGCKAFPKRSIQGH | 180 |
| QY | 181 | NDVI CPATNQCTIDKNRKSQAQCLRKCYEVMGVKQSRREERCGLVVRQRSADEQLH | 240 |
| DB | 181 | NDVI CPATNQCTIDKNRKSQAQCLRKCYEVMGVKQSRREERCGLVVRQRSADEQLH | 240 |
| QY | 241 | CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAPPVHLISRPSPAFFTEASMMSLTK | 300 |
| DB | 241 | CAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAPPVHLISRPSPAFFTEASMMSLTK | 300 |
| QY | 301 | LADKLVEHMISWAKKIPG 318 | |
| DB | 301 | LADKLVEHMISWAKKIPG 318 | |
| RESULT 6 | | | |
| ID | Q90ZE6 | PRELIMINARY; | PRT; 542 AA. |
| AC | Q90ZE6; | | |
| DT | 01-DEC-2001 (TREMBlrel. 19, Created) | | |
| DT | 01-DEC-2001 (TREMBlrel. 19, Last sequence update) | | |


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Db 436 GGELOGRSKLLCLDSDVTDALWAIKSTGLSFQORSTRHLAHLMLLSHRHNSKGMNDH 495
Qy 476 LANKKXNVVPVYDLEMLNAHVLROCKSITGSECSA-EDSKSGEQSONPOSQ 530
Db 496 LHCXMKKQVPLVYDLEMLDAHIMSHSLSHSGPRAAPAPKESKGVQEQALTRTSQ 551

RESULT 9
Q7ZU32
ID Q7ZU32 PRELIMINARY; PRT; 553 AA.
AC Q7ZU32;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Esr2a protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044349; RAH44349.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000536; Hormone rec lig.
DR InterPro; IPR001723; Steroid receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STROIDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI_1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
SQ SEQUENCE 553 AA; 62339 MW; 1E7E78AB6AD7A53 CRC64;

Query Match 51.9%; Score 1455.5; DB 13; Length 553;
Best Local Similarity 55.7%; Pred. No. 8.3e-125;
Matches 290; Conservative 78; Mismatches 126; Indels 27; Gaps 9;

Qy 16 YNCOSILPLEHGSIVPSSYDSSHHEYPAMTFYSPAVKNSIP--SNVTNLEGGFGQRT 73
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DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR KX DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc; Zinc-finger.
KX TRANSCRIPTION_REGULATION; ZINC_ZINC_FINGER.
SQ SEQUENCE 553 AA; 61.9% ID, 84C4DE67AC0C5ED CRC64;

Query Match      51.9%; Score 1454.5; DB 13; Length 553;
Best Local Similarity 55.7%; Pred. Co. 1e-124;
Matches 290; Conservative 78; Mismatches 126; Indels 27; Gaps 9;

QY 16 YNCQSQTLPLEHSGSIYIPSSVDSHSEYPAMTFYSPAVMVSIP--SNVTLEGPGGROT 73
DB 31 FNSGSSELPLEVENHPICIPSPITDGLGHDFSTLFFYSPLLGYSTSPFLDCSSV-----RQS 85
QY 74 TSNVLWPTFGHLSPLVVHRQLSHLYAEPQKSPCEARSLSEHTPLPVNRETLKRKVSGNRC 133
DB 86 LSPTLFWPPPHSVSSLTQQSRLLQQNHATSGTWTEHPDHVEEENSKLPIKGVADTEE 145
QY 134 ASPVTGPGSKRDAAFCVAGSDYASGYHYGVMSCEGCKAFFKRSIQGENDYICPATNOCTI 193
DB 146 TS--VSLRGKADMHYCAVCSDYASGYHYGVMSCEGCKAFFKRSIQGENDYICPATNOCTI 203
QY 194 DKNERKSCQACRLRKCYEVGMVKCGSRERRCYLRVRQRSADEQ---LHCAGAKRKGSGH 251
DB 204 DKNERKSCQACRLRKCYEVGMVKCGSRERRSY---QORGAQOKRLVPFSGRMRWTGPR 259
QY 252 APRVR-----ELLDALSPQLVLTLEAEPPHV-LISRSAPFTFASVMWSLTKL 301
DB 260 SQEIKSIPRPLSGNVGIVRIISPELISIRIMEAEPPFIYLMKMCKPTEANVMWSLNL 319
QY 302 ADRELVHMISWAKKI PGFVELSLFDQVRLLESCHMEVLMGLMWRSIDHPGKLIFAPDLV 361
DB 320 ADRELVHMISWAKKI PGFVELSLFDQVHLLCCWLEVLMLGLMWSYNHPGKLIFSPDLS 379
QY 362 LDRDEGKCVEGILFI DMILLATTGRTFRELKLOHKYLCVKAMILINSKW-YPLVTATODA 420
DB 380 LSRRDESCVQGLVEIFDMIIAATSFRFRELKLOREYVCLKAMILINSWCISSESSEGGSDL 439
QY 421 DSSEKLAHLNAVTDALVVWIAKSGISSQQOSMBLANLLMLSHVRASNKGMEHLNMK 480
DB 440 QSRKKLCLDSVDTDALVWAISKTLGSLFQQRSSTRLAHLMLSHIRHVSNKGDHRLCMK 499
QY 481 CKNVVPVYDLLLEMLNAHVLRCGCKSSITGSECSPA-EDSKS 520
DB 500 MKQWPVLYDLLLEMDAHIMESSRLSHSGPPAPAHHKDKS 540

RESULT 11
Q8AV62 PRELIMINARY; PRT; 553 AA.
AC O8AV62;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Estrogen receptor beta a.
OS Brachydanio rerio (Zebrafish) [Danio rerio].
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22347324; PubMed=12459262;
RA Lassiter C.S., Kelley B., Linney E.;
RT "Genomic Structure and Embryonic Expression of Estrogen Receptor Beta
a (ERbeta a) in Zebrafish (Danio rerio).";
Re Gene 299:141-151(2002).
DR EMBL; AF516874; AAN60793.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
```

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR008946; Str_ncl_receptor.
InterPro; IPR001628; Znf_Casteroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STROHORMONER.
PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_Casteroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor.
XW
SQ SEQUENCE 553 AA; 62196 MW; 928FC9E0D339844B CRC64;

Query Watch 51.4%; Score 1441.5; DB 13; Length 553;
Best Local Similarity 55.3%; Pred.No.1.6e-123;
Matches 288; Conservative 76; Mismatches 130; Indels 27; Gaps 9

| | | | |
|----|-----|--|-----|
| QY | 16 | YNCSQSILPLSHGSGIYIPSSVVDSSHYPAMTIFYSPAVMNYISIP--SNVTNLEGGPGROT | 73 |
| DB | 31 | FNSSPSPLPVENHPICPSPYTDLGHDFSTLPFYSPALLGYSTSPLSDCSSV-----RQS | 85 |
| QY | 74 | TSPNVLVTFPHGLSLPVVHRQLSHLYAEPOKSWCEARSLEHTLPVNRETLKKEYSGNEC | 133 |
| DB | 86 | LSFTFLFWPHSHVSLSLTQQOSRLQQNHATSGTWTEHTPDHVVEENSPLVKPVAETEE | 145 |
| QY | 134 | ASPVTPGCSKDADFCAVCSDYASGYHYGVNSCGCKAPFKRSIQGHNDYICPATNQCTI | 193 |
| DB | 146 | TS--VSLRGADMYCAVSDYASGYHYGVNSCGCKAPFKRSIQGHNDYICPATNQCTI | 203 |
| QY | 194 | DKNRKSCQACLRRCKYEVMVGKCSRRRCGRVLVRORSDEQ--LECAGKAKRSGGH | 259 |
| DB | 204 | DKNRKSCQACLRRCKYEVMVGKCSRRRSSY----QQRGAQQKLIVFSGRGMTGPR | 259 |
| QY | 252 | ARVREL-----LLDALSPQALVLTILEARPPHV-LISRESAPFFTEASMMSLTKL | 301 |
| DB | 260 | SQEIKSPIRPLSGNEGARISUSPELISRMEARPPFIYLKMDKPFTEANVMSLTNL | 319 |
| QY | 302 | ADKELVHMISWAKTIPIGFVELSLFDQVRLLESCEMVLMGLMWRSIDIHGKLIIFAPDLV | 361 |
| DB | 320 | ADKELVHMISWAKTIPIGFVELSLFDQVRLLECCWLLEVLMGLMWRSVNHGPKLIIFS | 379 |
| QY | 362 | LORDGKCVEGIIEIFDMILLATTSPREKLKHKEYLCVKAMILLNSSM-YPLVATODA | 420 |
| DB | 380 | LSRDESSCQGLVEIFDMILLAASTRPREKLQKREYVCLKAMILLNNMLCASSEGEDU | 439 |
| QY | 421 | DSSRLKHLNAVTDALVWVIATAKGISQQOOSRELANLMLLSHVRHASKNGHEHLNMK | 480 |
| DB | 440 | QRSKLKLLDSVTDALVWLSKTGLSFQQRSTFLAHLMLLSHIRVSKMGDHLHKMK | 499 |
| QY | 481 | KRNVPVPTDLLLEMLNAHLRGCKSSITGCSECPA-EDSKS | 520 |
| DB | 500 | MKKMAPLYDLLLEMLDAHIMESSLSHSGPRAPAHHKNKS | 540 |

RESULT 12

| ID | Q8QHKG | PRELIMINARY; | PRT: | 565 AA. |
|----|--|---|------|---------|
| AC | Q8QHKG; | | | |
| DT | 01-JUN-2002 | (TREMBLrel. 21, Created) | | |
| DT | 01-JUN-2002 | (TREMBLrel. 21, Last sequence update) | | |
| DT | 01-OCT-2003 | (TREMBLrel. 25, Last annotation update) | | |
| DE | | Estrogen receptor beta. | | |
| GN | ERA. | | | |
| OS | Paralichthys olivaceus (Flounder). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; | | | |
| OC | Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; | | | |
| OC | Pleuronectoidei; Paralichthyidae; Paralichthys. | | | |
| OX | NCBI_Taxid=8255; | | | |
| RN | [1] | | | |

| | |
|--------|-------|
| RESULT | 12 |
| Q8QH9 | Q8QH9 |
| ID | AC |
| DT | DT |
| DT | DT |
| DT | DT |
| DE | ERB: |
| GN | Para |
| OS | Euka |
| OC | Acti |
| OC | Acan |
| OC | Pleu |
| OX | NCBI |
| RN | [1] |

DE Estradiol receptor beta a.
DS Brachydanio rerio (Zebrafish) (Danio rerio).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22347324; PubMed=12459262;
RA Lassiter C.S., Kelley B., Linney E.;
RT "Genomic Structure and Embryonic Expression of Estrogen Receptor Beta
a (ERbeta a) in Zebrafish (Danio rerio).";
Rf Gene 299:141-151 (2002).
Ri ENEL; AF516874; AAN60793.1; -;
DR GO: 0005634; C:nucleus; IEA.
DR GO: 0003707; F:steroid hormone receptor activity; IEA.
DR GO: 0003700; F:transcription factor activity; IEA.

K9 PRELIMINARY; PRT; 565 AA.
K3;
UN-2002 {T-EMBLrel. 21, Created}
UN-2002 {T-EMBLrel. 21, Last sequence update}
TUN-2003 {T-EMBLrel. 25, Last annotation update}
ogen receptor beta.
plichthys olivaceus (Flounder).
Xryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Neopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Thomomys; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectidae; Paralichthyidae; Paralichthys.
_TaxID=8255;

| | | |
|---|--|--|
| RP | SEQUENCE FROM N.A. | |
| RA | Kitano T., Sakimura N., Takamune K., Nagahama Y., Abe S.: "Role of estrogen receptor in gonadal sex differentiation in Japanese flounder (Paralichthys olivaceus)."; | |
| RT | Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases. | |
| CC | -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). | |
| CC | -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY. | |
| DR | EMBL; AB070630; BAB85623.1; - | |
| DR | HSSP; P19793; 1LBD. | |
| DR | GO; GO:0005634; C:nucleus; IEA. | |
| DR | GO; GO:0005524; P:ATP binding; IEA. | |
| DR | GO; GO:0005489; F:steroid hormone receptor activity; IEA. | |
| DR | GO; GO:0003707; F:transcription factor activity; IEA. | |
| DR | GO; GO:0003700; F:electron transport; IEA. | |
| DR | GO; GO:0006118; P:electron transport; IEA. | |
| DR | GO; GO:0006355; P:proton transport; IEA. | |
| DR | GO; GO:0006350; P:transcription; IEA. | |
| DR | InterPro; IPR000194; ATPase_a/bcentre. | |
| DR | InterPro; IPR000345; CytC_heme_BS. | |
| DR | InterPro; IPR000536; Hormone_rec_lig. | |
| DR | InterPro; IPR001723; Stdhrmn_receptor. | |
| DR | InterPro; IPR008946; Str_ncl_receptor. | |
| DR | InterPro; IPR001628; Znf_C4steroid. | |
| DR | Pfam; PF00104; hormone_rec; 1. | |
| DR | Pfam; PF00105; zf-C4; 1. | |
| DR | PRINTS; PR00398; STRDHORMONER. | |
| DR | PRINTS; PR00047; STROIDFINGER. | |
| DR | ProDom; PD000035; Znf_C4steroid; 1. | |
| DR | SMART; SM00430; HOL1; 1. | |
| DR | SMART; SM00399; Znf_C4; 1. | |
| DR | PROSITE; PS00152; ATPASE_ALPHA_BETA; 1. | |
| DR | PROSITE; PS00031; NUCLEAR_RECEPTOR; 1. | |
| DR | PROSITE; PS00190; CYTOCHROME_C; 1. | |
| KW | DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription; Transcription regulation; Zinc; Zinc-finger. | |
| KW | Transcription regulation; Zinc; Zinc-finger. | |
| SQ | SEQUENCE 565 AA; 62521 MW; 74CAB8E1426B8D7 CRC64; | |
| Query Match 50.3%; Score 1410.5; DB 13; Length 565; | | |
| Best Local Similarity 54.5%; Pred. No. 1.2e-120; | | |
| Matches 291; Conservative 66; Mismatches 146; Indels 31; Gaps 12; | | |
| Qy | 9 SLNPS-SYNGSQSLPLEHSGSIYIPSSYVDSHHEYPAMTYSPAVMNYISIPSNVTLLEG 67 | |
| Db | 33 STSSFLGLDGSQPC-----IPSPYTELGHDFATIPFVGPIPSYAAPS---IPD 80 | |
| Qy | 68 GPG-ROTPSPNVLWPTPGHLS-PLVVHR-QLSHLYAEQKSPWCEARSLHTLPVNRHTL 124 | |
| Db | 81 CPVHQSLSPLEWPSHGHGMPMTLHRSQGRSQGQPIQSPFWGELTPRDGVL-ANSKGV 139 | |
| Qy | 125 KRKSGNRCASPVTPGSKRDAHFCVACSDYASGYHYGVWCEGCKAFFKRSIQCHNDYI 184 | |
| Db | 140 RRR--SQESDGVSSGGKSDLHYCAVCHDYASGYHYGVWCEGCKAFFKRSIQCHNDYI 197 | |
| Qy | 185 CPATNQCTIDKNNRKSQACRLKCYEYGVWVKGSRRCRGYR--LVRRQSADEQLHCA 242 | |
| Db | 198 CPATNQCTIDKNNRKSQACRLKCYEYGVWVKGSRRCRGYR--LVRRQSADEQLHCA 257 | |
| Qy | 243 GKAKESGGAHPRVRELLDALSPEQLVTLLEAEPPHY-LISRPAPTEASMMWLSITKL 301 | |
| Db | 258 GKALTGPVVALMNEQLPALTPEQLIERIMEAEPPIVLYMKMSGPLTEANVMSLTHL 317 | |
| Qy | 302 ADKELVHMI-SNAKTI-PGVFVLSLFDQVRLLESCKWNEVLMGLMWSRIDHPKLI-FADPLV 361 | |
| Db | 318 ADKELVHMI-TWAKTI-PGVFVLSLFDQVRLLESCKWNEVLMGLMWSRIDHPKLI-FSPDLS 377 | |
| Qy | 362 LDRDRGKVEGLETFDMLLATTSPREKLQHKYLCVKAMILLNSM-YPLVTATODA 420 | |
| Db | 378 LSREGSCVQGSSEIFDMLIAATSPREKLQHKYLCVKAMILLNSM-YPLVTATODA 437 | |
| Qy | 421 DSSRLKLAHLNVAITDALVVTAKSGISSQQQSMELANILLMLSHVTHASNKGMBHLANK 480 | |
| Db | 438 HSRSKLLILLDAVTDALVWIAKTGLTFRQOVTRLAHLMLLISHIRVSNKGMDBLHCKM 497 | |

| | | |
|---|---|--|
| Qy | 481 CRNVVPPVYDILLLEMLNAHVLRGCK-----SSITGSECSPAEDSKSKGSGSN 526 | |
| Db | 498 MKNNVPLDILLLEMLNAHVLRGCK-----SSITGSECSPAEDSKSKGSGSN 551 | |
| RESULT 13 | | |
| Q804Q7 | PRELIMINARY; PRT; 553 AA. | |
| AC | Q804Q7; (T-EMBLrel. 24, Created) | |
| DT | 01-JUN-2003 (T-EMBLrel. 24, Last sequence update) | |
| DT | 01-OCT-2003 (T-EMBLrel. 25, Last annotation update) | |
| DB | Estrogen receptor beta. | |
| OS | Acanthopagrus schlegelii (Black porgy). | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC | Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; | |
| OC | Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae; | |
| OC | Spuridae; Acanthopagrus. | |
| OX | NCBI_TaxID=72011; | |
| RN | [1] | |
| RP | SEQUENCE FROM N.A. | |
| RC | T-SSUE=Ovary; | |
| RA | Huang Y.-S., Yueh W.-S., Huang J.-D., Du J.-L., Sun L.-T., | |
| RA | Nagahama Y., Chang C.-F.; | |
| RT | "Cloning and Expression of Estrogen Receptors in the Protandrous Black Porgy (Acanthopagrus schlegelii): Implication of Sex Change Mechanism."; | |
| RL | Mar. Biotechnol. 4:236-246(2002). | |
| DR | EMBL; AY074779; AAL82742.1; - | |
| DR | GO; GO:0005634; C:nucleus; IEA. | |
| DR | GO; GO:0005524; F:ATP binding; IEA. | |
| DR | GO; GO:0005489; F:electron transporter activity; IEA. | |
| DR | GO; GO:0003707; F:steroid hormone receptor activity; IEA. | |
| DR | GO; GO:0003700; P:transcription factor activity; IEA. | |
| DR | GO; GO:0006118; P:electron transport; IEA. | |
| DR | GO; GO:0015992; P:proton transport; IEA. | |
| DR | GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA. | |
| DR | InterPro; IPR000194; ATPase_a/bcentre. | |
| DR | InterPro; IPR000345; CytC_heme_BS. | |
| DR | InterPro; IPR000536; Hormone_rec_lig. | |
| DR | InterPro; IPR001723; Stdhrmn_receptor. | |
| DR | InterPro; IPR008946; Str_ncl_receptor. | |
| DR | InterPro; IPR001628; Znf_C4steroid. | |
| DR | Pfam; PF00104; hormone_rec; 1. | |
| DR | Pfam; PF00105; zf-C4; 1. | |
| DR | PRINTS; PR00398; STRDHORMONER. | |
| DR | PRINTS; PR00047; STROIDFINGER. | |
| DR | ProDom; PD000035; Znf_C4steroid; 1. | |
| DR | SMART; SM00430; HOL1; 1. | |
| DR | SMART; SM00399; Znf_C4; 1. | |
| DR | PROSITE; PS00152; ATPASE_ALPHA_BETA; 1. | |
| DR | PROSITE; PS00190; CYTOCHROME_C; 1. | |
| DR | PROSITE; PS00031; NUCLEAR_RECEPTOR; 1. | |
| KW | Receptor. | |
| SQ | SEQUENCE 553 AA; 61953 MW; 7CC094638CBE4AA2 CRC64; | |
| Query Match 50.2%; Score 1409.5; DB 13; Length 553; | | |
| Best Local Similarity 52.9%; Pred. No. 1.4e-120; | | |
| Matches 286; Conservative 71; Mismatches 133; Indels 51; Gaps 12; | | |
| Qy | 3 IKSPSSLSNPSYVDSHHEYPAMTYSPAVMNYISIPSNV 62 | |
| Db | 29 VLSPMETNTP-----ICIPSPYTRGHDFPALFPSPINFSYANPPI 72 | |
| Qy | 63 TNLGGSPGROTTSPNVLWPTPGHLSPLVHRQSHLYAEQKSPWCEARSLHTL 117 | |
| Db | 73 SDRPS--VHQTLSSSLFWPSHGHVGTTL---PLHLOARPHQHGQVQSPWVLSPLDNVL 127 | |
| Qy | 118 PVNRETLARKVSGNRCASPVTPGSKEDAHFACVDSYASGYHYGVWCEGCKAFFKRSI 177 | |
| Db | 128 TSSKASRR---SQESSEGEVSSGGKADLHFCVCHDYASGYHYGVWCEGCKAFFKRSI 184 | |

QY 178 QGHNDYICPATNQCTIDKNRKSQACRLKCYEYGVKSGRRRCGYRLVRRORSAD 237
Db 185 QHNDYICPATNQCTIDKNRKSQACRLKCYEYGVKSGRRRCGYRLVRRORSAD 242
QY 238 QHCHAGKAKRSGHAPRVRELL---DALSPQLVLTLEABPPHV-LISPSAPPTAS 293
Db 243 RLSSQGT-----NGPVGELIAPOPALTSKQLIERIEABPPHYLMKVRRLPTAN 297
QY 294 NMMSLTKLADKELVHMISWAKKIPGVFELSDFDQVRLLESQMEVLMGLMWSIDHPGK 353
Db 298 IMMSLTNLADKELVHMISWAKKIPGVFELSDFDQVRLLESQMEVLMGLMWSIDHPGK 357
QY 354 LIPAPDLVDRDEKGVCEGILIFDMLATTGRFRELKLOHKEYLCVQKAMILLNSM-YP 412
Db 358 LIFSPDLSLRBEGSCVQGFIFDMLIAATSRVRELKLOHKEYLCVQKAMILLNSMCLS 417
QY 413 LVTATODADSSKLAHLNAVTDALVWIAKSGISSQOOSMELANMLLSHVRHASNKG 472
Db 418 SEGSELSQSKLELLDAVTDALVWIAKSGISSQOOSMELANMLLSHVRHASNKG 477
QY 473 MEHLNLMKCNVVPVVDLLEMLNAHVL-----RGCKSSITGSECSPAEDSKSKEGQN 526
Db 478 MDHLGMKKNVPLYDLEMLDAHIMHSSRLPRSPQOETGDCQ-----DGPAPRHPG 533
QY 527 P 527
Db 534 P 534
RESULT 14
Q7T2K7 PRELIMINARY; PRT; 671 AA.
AC Q7T2K7
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Estrogen receptor beta.
OS Halichoeres tenuispinis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
OC Labridae; Halichoeres.
OX NCBI_TaxID=217853;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Liver;
RC Tissue=Liver;
RA Park J.-G., Kim S.-J.;
RT "Molecular cloning and expression of two estrogen receptor subtypes in
protogynous wrasse, Halichoeres tenuispinis."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AV305027; AAP72179.1; -
KW Receptor.
SQ SEQUENCE 671 AA; 74781 MW; 5373F8129DF71C6A CRC64;
Query Match 49.9%; Score 1401; DB 13; Length 671;
Best Local Similarity 52.4%; Pred. No. 1.1e-119;
Matches 300; Conservative 73; Mismatches 127; Indels 72; Gaps 17;
QY 5 NSPSSINSPSNCQSILPLEHSGIYIPSSVYDSHVEY-----PAMTEYSPAVMYNYSIPS 60
Db 30 SSPGLL--PAVYSPRGQ---MDSHYITPSPYDNNQYHMGSGSVSFSPSVLSTARS 84
QY 61 NVTNLEG--QPGRQITSPNVLNFTPGHLSPLVVRQL-----SHLYAEPPQKSPNC 108
Db 85 ATDPSPLSGP---LSPSAFWPP--HSQNLPLSLTLRCPOPLGVNYESGLHA-----PWL 133
QY 109 EAR-----SLEHTLPVNRRETLKRVSG-----NRCSPTVPGSKVEDAFCHVCSQDYS 157
Db 134 ESKPHNISSSSSSICGNKPKGRKSEBGNVGNPFLSSSVV-----GRADMEFCAVCHDYS 189
QY 158 GYHYGVWSCGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQACRLKCYEYGVKMK 217
Db 190 GYHYGVWSCGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQACRLKCYEYGVKMK 249

QY 218 GSRRRCGYRLVRRORS-----ADQLHCAGKAKSGGH-----APRVREL 258
Db 250 GVRERCSTGRHRRGGLQPRDPTGRGLVVRGLSRAQRHLHLEGPLTPTVPLPQMSHV 309
QY 259 LLDALSPQLVLTLEABPPHV-LISPSAPPTASNMMSLTKLADKELVHMISWAKKIP 317
Db 310 HHAAMSPEEFIMRINEAPEPEIYLMEEQKPFTEASNMMSLTNLADKELVHMISWAKKIP 369
QY 318 GFVELSDFDQVRLLESQMEVLMGLMWSIDHPGKLIFFAPDLVDRDEKGVCEGILIF 377
Db 370 GFVELCLADQHLHLLKCCWLEILMLGLMWSVDHPGKLIFSPDFKLNREEGQCVGIMEIF 429
QY 378 DMLATTGRFRELKLOHKEYLCVQKAMILLNSMTPVTAT--QDADSSKLAHLNAVTD 436
Db 430 DMLAATSRFRELKLOHKEYLCVQKAMILLNSLNCSSPQTEEBELESNRKLRJLDSVID 489
QY 437 LVWIAKSGISSQOOSMELANMLLSHVRHASNKGMEHLNLMKCNVVPVVDLLEMLN 496
Db 490 LVWIAKSGILSTQOQTLRLGLHLLSHIRHVSNGKMDHLSMKRKNVVLVVDLLEMLD 549
QY 497 AHVLRGCKSSITGSECSPAEDSKSKEGQNPO 528
Db 550 ANT---SSSGSSQSSSSPNSDYS-DLHQYPO 577
RESULT 15
Q9OWS9 PRELIMINARY; PRT; 592 AA.
AC Q9OWS9
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ZFER-beta1 protein.
GN ZFER-BETA1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Menuet A., Pellegri E., Anglade I., Blaise O., Laudet V., Kah O.,
RA Pakdel F.;
RT "Binding characteristics, transactivation properties and central
expression of three estrogen receptor subtypes in zebrafish."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL: AJ414566; CAC93848.1; -
DR HSP: P19793; 1LBD.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0005489; P:electron transporter activity; IEA.
DR GO: GO:0003707; P:steroid hormone receptor activity; IEA.
DR GO: GO:0003700; P:transcription factor activity; IEA.
DR GO: GO:0006118; P:regulation of transcription; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR000345; CytC_heme_BS.
DR InterPro: IPR000336; Hormone_rec_lig.
DR InterPro: IPR001723; Steroid_receptor.
DR InterPro: IPR008946; Str_ncl_receptor.
DR InterPro: IPR001628; Znf_C4steroid.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PR00398; STRDHORMONER.
DR PRINTS: PR00047; STROIDFINGER.
DR ProDom: PD000035; Znf_C4steroid; 1.
DR SMART: SM00430; HOLI_1.
DR SMART: SM00399; Znf_C4; 1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;

KW Transcription regulation: Zinc; Zinc-finger.
SQ SEQUENCE 592 AA; 66046 MW; 7F65218E2C03F1B8 CRC64;

Query Match 49.8%; Score 1397.5; DB 13; Length 592;
Best Local Similarity 51.6%; Pred. No. 1.9e-119;
Matches 300; Conservative 79; Mismatches 121; Indels 81; Gaps 16;

QY 11 NSPSYNCOSQILP-----LEHGSYIPSSVYDSHSEYP-----AMTFYSP- 51
DB 13 SSKADRGASPALPLLYASPLGMDNQTCIPSPYACADYSPHGGEFNGHGLTLYSPV 72

QY 52 --AVNYSIPSNVNTNLEGGQRQTTSPNVLPTPGHL---SPLVVHQLSHLYABPOKSP 106
DB 73 SSAVLGFRFRPPVSESL-----VPLSPTILWP-PHSLHCPPLAYSETRSH-----SA 118

QY 107 WCEARSLHTLPVNRKTLK-----RVSGNRKASPTVPGSKRDAPHCAVCSYASGYH 160
DB 119 WEEKAT--HTLSQSSVLSHTKLLCQQLGNGNLPSASIVGKGDTHTFCAVCHDYASGYH 176

QY 161 YGVNSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQACRLRKCXYEVMVKCGSR 220
DB 177 YGVNSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQACRLRKCXYEVMVKCGVR 236

QY 221 RERCYRLVRQR-----SADEQLHCAGKAKR-----SGGHAPRVRELL 260
DB 237 RERCYRGARHRNPQIRDSSGVVGLRGQSOHLEPPLSPSOHLFPSCGRA-EGRAL-- 293

QY 261 DALSPQLVLTLEAPPHVLISRP-SAPFTEASMMSLTKLADKELVHMISWAKKIPGF 319
DB 294 -NYSPEQLVSCILEAPPOIVLREPVKPYTEASMMSLTSLADKELVLMISWAKKIPGF 352

QY 320 VELSLFDQVRLLESCWMEVLMGLMWSRIDHKGKLIAPDLVLDDEGCKVEGILEIFDM 379
DB 353 VELTSLDQVHLLECWLIDILMGLMWSVDHPGKLIPTDCLKAREGNCVEGIMBIFDM 412

QY 380 LLATTSRRELKQHKYLCVKAMILLNSMYPLVTAT-QDADSSRKLALHNAVTDALV 438
DB 413 LLATTSRRELKQREYVCLKAMILLNSNCSLPQTPEDVESRGKVLNLDSDVTDALV 472

QY 439 WVIKSGISSQOOSRLANLLMLLSHVHSAKNGHEHLNNKCKNVVPPVYDILLEMNAH 498
DB 473 WIISTRGLSSQOOSTIRLAHLLMLLSHIRLSNKGIEHLSNKKRNKVVLLYDILLEMLDAN 532

QY 499 VLRGCK-----SSITGSECSFAEDSKSGSQNFQSQ 530
DB 533 ASQSRMLEDRQOSPENLHTSRPQDLDKDSQETPHSPRAE 573

Search completed: June 20, 2004, 10:38:38
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2004, 10:36:03 ; Search time 23 Seconds
 (without alignments)
 1189.642 Million cell updates/sec

Title: US-08-906-365-2
 Perfect score: 2805
 Sequence: 1 MDIKNSPSSLNSSSYNCQS.....ECSPABDSKSKESQNPQSQ 530

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:*
 1: /cgm2_6/ptodata/2/iaa/5A COMB.pep.*
 2: /cgm2_6/ptodata/2/iaa/5B COMB.pep.*
 3: /cgm2_6/ptodata/2/iaa/6A COMB.pep.*
 4: /cgm2_6/ptodata/2/iaa/6B COMB.pep.*
 5: /cgm2_6/ptodata/2/iaa/PTCUS COMB.pep.*
 6: /cgm2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------|
| 1 | 2805 | 100.0 | 530 | 4 | US-09-608-088-25 |
| 2 | 2805 | 100.0 | 548 | 3 | US-09-139-617-1 |
| 3 | 2805 | 100.0 | 548 | 4 | US-09-561-741A-1 |
| 4 | 2805 | 100.0 | 548 | 2 | US-09-558-795-1 |
| 5 | 2554 | 91.1 | 485 | 2 | US-08-836-620A-3 |
| 6 | 2522 | 89.9 | 477 | 4 | US-09-608-088-5 |
| 7 | 2291 | 81.7 | 485 | 2 | US-08-836-620A-2 |
| 8 | 2286 | 81.5 | 484 | 2 | US-08-836-620A-13 |
| 9 | 2267 | 80.8 | 485 | 2 | US-08-836-620A-5 |
| 10 | 2262 | 80.6 | 484 | 2 | US-08-836-620A-14 |
| 11 | 2198 | 78.4 | 416 | 4 | US-09-608-088-6 |
| 12 | 2198 | 78.4 | 418 | 4 | US-09-608-088-21 |
| 13 | 2017 | 71.9 | 384 | 2 | US-08-836-620A-15 |
| 14 | 1233.5 | 44.0 | 595 | 3 | US-08-870-12 |
| 15 | 1233.5 | 44.0 | 595 | 3 | US-08-980-115-12 |
| 16 | 1224.5 | 43.7 | 595 | 3 | US-09-041-886-35 |
| 17 | 1224.5 | 43.7 | 595 | 4 | US-08-453-988-2 |
| 18 | 1222.5 | 43.6 | 595 | 2 | US-08-836-620A-17 |
| 19 | 1214.5 | 43.3 | 596 | 2 | US-08-836-620A-16 |
| 20 | 1181 | 42.1 | 233 | 4 | US-09-608-088-4 |
| 21 | 1160 | 41.4 | 410 | 6 | 5223606-5 |
| 22 | 1136.5 | 40.2 | 229 | 3 | US-09-249-645-1 |
| 23 | 1111.5 | 39.6 | 229 | 4 | US-09-844-132B-1 |
| 24 | 1064 | 37.9 | 228 | 3 | US-09-249-645-2 |
| 25 | 1064 | 37.9 | 228 | 4 | US-09-844-132B-2 |
| 26 | 1055 | 37.6 | 226 | 2 | US-08-836-620A-7 |
| 27 | 810 | 28.9 | 773 | 3 | US-08-564-264-1 |

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|----|-------|------|-----|---|-------------------|--------------------|
| 28 | 762 | 27.2 | 651 | 3 | US-08-693-940-3 | Sequence 3, Appli |
| 29 | 762 | 27.2 | 651 | 4 | US-09-566-660-3 | Sequence 3, Appli |
| 30 | 746.5 | 26.6 | 264 | 4 | US-09-660-979-1 | Sequence 1, Appli |
| 31 | 668.5 | 23.8 | 243 | 2 | US-08-836-620A-9 | Sequence 9, Appli |
| 32 | 666 | 23.7 | 243 | 2 | US-08-836-620A-8 | Sequence 8, Appli |
| 33 | 660.5 | 23.5 | 243 | 2 | US-08-836-620A-10 | Sequence 10, Appli |
| 34 | 648 | 23.1 | 435 | 3 | US-09-040-508-2 | Sequence 2, Appli |
| 35 | 648 | 23.1 | 435 | 3 | US-09-500-654-2 | Sequence 4, Appli |
| 36 | 648 | 23.1 | 438 | 3 | US-09-141-000-4 | Sequence 2, Appli |
| 37 | 630 | 22.5 | 500 | 3 | US-09-141-000-2 | Sequence 2, Appli |
| 38 | 627.5 | 22.4 | 431 | 2 | US-08-836-620A-19 | Sequence 19, Appli |
| 39 | 588.5 | 21.0 | 518 | 2 | US-08-836-620A-18 | Sequence 18, Appli |
| 40 | 576 | 20.5 | 418 | 3 | US-09-141-000-6 | Sequence 6, Appli |
| 41 | 460.5 | 16.4 | 525 | 3 | US-08-764-870-7 | Sequence 7, Appli |
| 42 | 460.5 | 16.4 | 525 | 3 | US-08-980-115-7 | Sequence 7, Appli |
| 43 | 459 | 16.4 | 446 | 1 | US-07-952-800-4 | Sequence 4, Appli |
| 44 | 458.5 | 16.3 | 533 | 1 | US-07-952-800-2 | Sequence 2, Appli |
| 45 | 458.5 | 16.3 | 533 | 4 | US-08-216-592A-4 | Sequence 4, Appli |

ALIGNMENTS

RESULT 1
 US-09-608-088-25
 ; Sequence 25, Application US/09608088
 ; Patent No. 6580368
 ; GENERAL INFORMATION:
 ; APPLICANT: Mosselman, Sietse
 ; APPLICANT: Dijkema, Rein
 ; TITLE OF INVENTION: No. 6680368el Estrogen Receptor
 ; FILE REFERENCE: O/96193 US/D1
 ; CURRENT APPLICATION NUMBER: US/09/608,088
 ; CURRENT FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 08/826,361
 ; PRIOR FILING DATE: 1997-03-26
 ; PRIOR APPLICATION NUMBER: EP 96203284.3
 ; PRIOR FILING DATE: 1996-11-22
 ; PRIOR APPLICATION NUMBER: EP 96200820.7
 ; PRIOR FILING DATE: 1996-03-26
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 25
 ; LENGTH: 530
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-608-088-25

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|-----------------------|--------|--|----------|------------|--------|--------|
| Query Match | 100.0% | Score | 2805 | DB 4 | Length | 530 |
| Best local Similarity | 100.0% | Pred. No. | 1.4e-291 | | | |
| Matches | 530 | Conservative | 0 | Mismatches | 0 | Indels |
| | | | | | | |
| Qy | 1 | MDIKNSPSSLNSSSYNCQSILPLEHSGSIYIPSSYVDSHHEYPAMTFYSPAVMNSIPS | 60 | | | |
| Db | 1 | MDIKNSPSSLNSSSYNCQSILPLEHSGSIYIPSSYVDSHHEYPAMTFYSPAVMNSIPS | 60 | | | |
| Qy | 61 | NVTNLGGPGROTTSPNVLWPTGHLSPVLVHQLSHLYAEPOKSPKCEARSLEHTLPVN | 120 | | | |
| Db | 61 | NVTNLGGPGROTTSPNVLWPTGHLSPVLVHQLSHLYAEPOKSPKCEARSLEHTLPVN | 120 | | | |
| Qy | 121 | RETLKRVKVGNCRCASPVTPGSGKRDHAFCAVCSDYASGHYGVMSCEGCKAFKRSIQGH | 180 | | | |
| Db | 121 | RETLKRVKVGNCRCASPVTPGSGKRDHAFCAVCSDYASGHYGVMSCEGCKAFKRSIQGH | 180 | | | |
| Qy | 181 | NDVICPATNCTIDKRRKSCQARLKCVEGVKVGKSGRRRCGYELVVRQBSADQLH | 240 | | | |
| Db | 181 | NDVICPATNCTIDKRRKSCQARLKCVEGVKVGKSGRRRCGYELVVRQBSADQLH | 240 | | | |
| Qy | 241 | CAGKAKRSGGHAPRVRELLLDALSPQLVLTLEASPPHVLISRPAFTFASNMMSLTK | 300 | | | |
| Db | 241 | CAGKAKRSGGHAPRVRELLLDALSPQLVLTLEASPPHVLISRPAFTFASNMMSLTK | 300 | | | |
| Qy | 301 | LADKELVHVMISWAKTKPGFVELSLFDQVRLLESQWMEVLMGLMWRSDH?GKLI?FAPDL | 360 | | | |

Db 301 LADKELVHMSWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDHPGKLIAPDPL 360
Qy 361 VLDRDEGKCVGILEIFDMLLATTSRFRELKQHEKYLCKVAMILLNSMYPLVTATQDA 420
Db 361 VLDRDEGKCVGILEIFDMLLATTSRFRELKQHEKYLCKVAMILLNSMYPLVTATQDA 420
Qy 421 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASNKGHEHLNKK 480
Db 421 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASNKGHEHLNKK 480
Qy 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
Db 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530

RESULT 2
US-09-139-617-1
; Sequence 1, Application US/09139617
; Patent No. 6222015
; GENERAL INFORMATION:
; APPLICANT: WILKINSON, HILARY
; TITLE OF INVENTION: ESTROGEN RECEPTOR
; FILE REFERENCE: 20047Y
; CURRENT APPLICATION NUMBER: US/09/139,617
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/058,271
; EARLIER FILING DATE: 1997-09-08
; EARLIER APPLICATION NUMBER: 60/060,520
; EARLIER FILING DATE: 1997-09-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 548
; TYPE: PRT
; ORGANISM: HUMAN
US-09-139-617-1

Query Match 100.0%; Score 2805; DB 3; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.5e-291;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIKNSPSSLNSSPSSYNCQSILPLEHGSIIYIPSSYVDSHHEYPAWNTFYSPAVNNYSIPS 60
Db 19 MDIKNSPSSLNSSPSSYNCQSILPLEHGSIIYIPSSYVDSHHEYPAWNTFYSPAVNNYSIPS 78
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Db 79 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPQKSPWCEARSLEHTLPVN 138
Qy 121 RETLKRKVSNGRCASPVTPGSKRDAHFCVCSDYASGTHYGVWSCGCKAFFKRSIQGH 180
Db 139 RETLKRKVSNGRCASPVTPGSKRDAHFCVCSDYASGTHYGVWSCGCKAFFKRSIQGH 198
Qy 181 NDYICPATNOCTIDKNRRKSCQACRLKCYEYGVWVKGSRRCRCYRLVRRQSADEQLH 240
Db 199 NDYICPATNOCTIDKNRRKSCQACRLKCYEYGVWVKGSRRCRCYRLVRRQSADEQLH 258
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Db 259 CAGKAKRSGCHAPRVRELLLDLSPQLVTLLEAEPHVLISRPSPAPPTASMMMSLTK 318
Qy 301 LADKELVHMSWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDHPGKLIAPDPL 360
Db 319 LADKELVHMSWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDHPGKLIAPDPL 378
Qy 361 VLDRDEGKCVGILEIFDMLLATTSRFRELKQHEKYLCKVAMILLNSMYPLVTATQDA 420
Db 379 VLDRDEGKCVGILEIFDMLLATTSRFRELKQHEKYLCKVAMILLNSMYPLVTATQDA 438
Qy 421 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASNKGHEHLNKK 480
Db 439 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASNKGHEHLNKK 498

Qy 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
Db 499 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 548
RESULT 3
US-09-561-741A-1
; Sequence 1, Application US/09561741A
; Patent No. 6458551
; GENERAL INFORMATION:
; APPLICANT: WILKINSON, HILARY
; TITLE OF INVENTION: ESTROGEN RECEPTOR
; FILE REFERENCE: 20047Y
; CURRENT APPLICATION NUMBER: US/09/561,741A
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/139,617
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/058,271
; PRIOR FILING DATE: 1997-09-08
; PRIOR APPLICATION NUMBER: 60/060,520
; PRIOR FILING DATE: 1997-09-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 548
; TYPE: PRT
; ORGANISM: HUMAN
US-09-561-741A-1

Query Match 100.0%; Score 2805; DB 4; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.5e-291;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDIKNSPSSLNSSPSSYNCQSILPLEHGSIIYIPSSYVDSHHEYPAWNTFYSPAVNNYSIPS 60
Db 19 MDIKNSPSSLNSSPSSYNCQSILPLEHGSIIYIPSSYVDSHHEYPAWNTFYSPAVNNYSIPS 78
Qy 61 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPQKSPWCEARSLEHTLPVN 120
Db 79 NVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRHQLSHLYAEPQKSPWCEARSLEHTLPVN 138
Qy 121 RETLKRKVSNGRCASPVTPGSKRDAHFCVCSDYASGTHYGVWSCGCKAFFKRSIQGH 180
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Qy 181 NDYICPATNOCTIDKNRRKSCQACRLKCYEYGVWVKGSRRCRCYRLVRRQSADEQLH 240
Db 199 NDYICPATNOCTIDKNRRKSCQACRLKCYEYGVWVKGSRRCRCYRLVRRQSADEQLH 258
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Qy 301 LADKELVHMSWAKKIPGFVLSLFDQVRLLSCWMEVLMGLMWRSDHPGKLIAPDPL 360
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Qy 361 VLDRDEGKCVGILEIFDMLLATTSRFRELKQHEKYLCKVAMILLNSMYPLVTATQDA 420
Db 379 VLDRDEGKCVGILEIFDMLLATTSRFRELKQHEKYLCKVAMILLNSMYPLVTATQDA 438
Qy 421 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASNKGHEHLNKK 480
Db 439 DSSRKLHLNNAVTDALVWVIKSGISSQOOSRELANILLMLSHVRHASNKGHEHLNKK 498
Qy 481 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 530
Db 499 CKNVVPVYDILLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSONPQSQ 548

RESULT 4
US-09-558-795-1

Sequence 1, Application US/09558795
Patent No. 6562592
GENERAL INFORMATION:
APPLICANT: WILKINSON, HILARY
TITLE OF INVENTION: ESTROGEN RECEPTOR
FILE REFERENCE: 20047Y
CURRENT APPLICATION NUMBER: US/09/558,795
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/139,617
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/058,271
PRIOR FILING DATE: 1997-09-08
PRIOR APPLICATION NUMBER: 60/060,520
PRIOR FILING DATE: 1997-09-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 548
TYPE: PRT
ORGANISM: HUMAN
US-09-558-795-1

Query Match 100.0%; Score 2805; DB 4; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.5e-291;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSNSPSSNCOSILPLEHGSYIIPSSVDSHHEYPANTFYSPAVMYSIPS 60
DB 19 MDIKNSPSSNSPSSNCOSILPLEHGSYIIPSSVDSHHEYPANTFYSPAVMYSIPS 78
QY 61 NVTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPQKSPACBARSLEHTLPVN 120
DB 79 NVTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPQKSPACBARSLEHTLPVN 138
QY 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHYGVMSCEGCKAPFKRSIQGH 180
DB 139 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHYGVMSCEGCKAPFKRSIQGH 198
QY 181 NYDICPATNCTIDKNRKSQACRLKCYEVGMVKGSGRRRCGYRLVRRQRSADQLH 240
DB 199 NYDICPATNCTIDKNRKSQACRLKCYEVGMVKGSGRRRCGYRLVRRQRSADQLH 258
QY 241 CAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPTEASMMWLSLK 300
DB 259 CAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPTEASMMWLSLK 318
QY 301 LADKELVHLMISWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLMWSRIDHPGKLI 360
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DB 379 VLDRDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMILLNSMYPVTATQDA 438
QY 421 DSSKLAHLNNAVTDALVVIKSGISSQQOSKRLANMLLSHVHASNKGMEHLNNK 480
DB 439 DSSKLAHLNNAVTDALVVIKSGISSQQOSKRLANMLLSHVHASNKGMEHLNNK 498
QY 481 CKNVVPYDILLEMNAHVLRGCKSSITGSECSPADSCKSKGEGSQ 530
DB 499 CKNVVPYDILLEMNAHVLRGCKSSITGSECSPADSCKSKGEGSQ 548

RESULT 5
US-08-836-620A-3
Sequence 3, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT: Orphan receptor
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-836-620A-3

Query Match 91.1%; Score 2554; DB 2; Length 485;
Best Local Similarity 99.8%; Pred. No. 9.7e-265;
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 MTFYSPAVMYSIPSNTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPQKS 105
DB 1 MTFYSPAVMYSIPSNTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPQKS 60
QY 105 PACEARSLEHTLPVNRRETLKRVKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHYGVMS 165
DB 61 PACEARSLEHTLPVNRRETLKRVKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHYGVMS 120
QY 166 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRKSQACRLKCYEVGMVKGSGRRRCG 225
DB 121 CEGCKAFFKRSIQGHNDYICPATNCTIDKNRKSQACRLKCYEVGMVKGSGRRRCG 180
QY 226 YLVRQRSADQLHCAKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRP 285
DB 181 YLVRQRSADQLHCAKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRP 240
QY 286 SAPFTEASMMWLSLKADKELVHLMISWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLM 345
DB 241 SAPFTEASMMWLSLKADKELVHLMISWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLM 300
QY 346 RSIDHPGKLI 405
DB 301 RSIDHPGKLI 360
QY 406 LNSSMYPVTATQDADSSKLAHLNNAVTDALVVIKSGISSQQOSKRLANMLLSHV 465
DB 361 LNSSMYPVTATQDADSSKLAHLNNAVTDALVVIKSGISSQQOSKRLANMLLSHV 420
QY 466 RHASNKGMEHLNNKCNVVPYDILLEMNAHVLRGCKSSITGSECSPADSCKSKGEGSQ 525
DB 421 RHASNKGMEHLNNKCNVVPYDILLEMNAHVLRGCKSSITGSECSPADSCKSKGEGSQ 480

RESULT 6
US-09-608-088-5
Sequence 5, Application US/09608088

Sequence 1, Application US/09558795
Patent No. 6562592
GENERAL INFORMATION:
APPLICANT: WILKINSON, HILARY
TITLE OF INVENTION: ESTROGEN RECEPTOR
FILE REFERENCE: 20047Y
CURRENT APPLICATION NUMBER: US/09/558,795
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/139,617
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/058,271
PRIOR FILING DATE: 1997-09-08
PRIOR APPLICATION NUMBER: 60/060,520
PRIOR FILING DATE: 1997-09-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 548
TYPE: PRT
ORGANISM: HUMAN
US-09-558-795-1

Query Match 100.0%; Score 2805; DB 4; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.5e-291;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDIKNSPSSNSPSSNCOSILPLEHGSYIIPSSVDSHHEYPANTFYSPAVMYSIPS 60
DB 19 MDIKNSPSSNSPSSNCOSILPLEHGSYIIPSSVDSHHEYPANTFYSPAVMYSIPS 78
QY 61 NVTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPQKSPACBARSLEHTLPVN 120
DB 79 NVTNLEGGPGRQTTSNVLWPTPGHLSPLVHRLSHLYAEPQKSPACBARSLEHTLPVN 138
QY 121 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHYGVMSCEGCKAPFKRSIQGH 180
DB 139 RETLKRKVSNGRCASPVTPGSKRDHAFCAVCSDYASGYHYGVMSCEGCKAPFKRSIQGH 198
QY 181 NYDICPATNCTIDKNRKSQACRLKCYEVGMVKGSGRRRCGYRLVRRQRSADQLH 240
DB 199 NYDICPATNCTIDKNRKSQACRLKCYEVGMVKGSGRRRCGYRLVRRQRSADQLH 258
QY 241 CAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPTEASMMWLSLK 300
DB 259 CAGKAKSGGHAPRVRELLLDALSPQLVLTLEAEPHVLISRPSPAPTEASMMWLSLK 318
QY 301 LADKELVHLMISWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLMWSRIDHPGKLI 360
DB 319 LADKELVHLMISWAKKIPGFVELSLFDQVRLLESQWMEVLMWGLMWSRIDHPGKLI 378
QY 361 VLDRDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMILLNSMYPVTATQDA 420
DB 379 VLDRDEGKCVGEILEIFDMLLATTSRPRELKLOHKEYLCVKAMILLNSMYPVTATQDA 438
QY 421 DSSKLAHLNNAVTDALVVIKSGISSQQOSKRLANMLLSHVHASNKGMEHLNNK 480
DB 439 DSSKLAHLNNAVTDALVVIKSGISSQQOSKRLANMLLSHVHASNKGMEHLNNK 498
QY 481 CKNVVPYDILLEMNAHVLRGCKSSITGSECSPADSCKSKGEGSQ 530
DB 499 CKNVVPYDILLEMNAHVLRGCKSSITGSECSPADSCKSKGEGSQ 548

RESULT 5
US-08-836-620A-3
Sequence 3, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT: Orphan receptor
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

Patent No. 6680368
GENERAL INFORMATION:
APPLICANT: Mosselman, Sietse
APPLICANT: Dijkema, Rein
TITLE OF INVENTION: No. 6680368el Estrogen Receptor
FILE REFERENCE: O/96193 US/DI
CURRENT APPLICATION NUMBER: US/09/608,088
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 08/826,361
PRIOR FILING DATE: 1997-03-26
PRIOR APPLICATION NUMBER: EP 96203284.3
PRIOR FILING DATE: 1996-11-22
PRIOR APPLICATION NUMBER: EP 96200820.7
PRIOR FILING DATE: 1996-03-26
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent in version 3.0
SEQ ID NO 5
LENGTH: 477
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-088-5

Query Match 89.9%; Score 2522; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.5e-261;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

54 MNYISPSNVNLEGGSGRQTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPKCRARSL 113
Db 1 MNYISPSNVNLEGGSGRQTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPKCRARSL 60

114 EHTLPVNRRETLKRVSGNRKASPTVPGSKRDAHFCAVCSDYASGYHYGWSCEGCKAFF 173
Db 61 EHTLPVNRRETLKRVSGNRKASPTVPGSKRDAHFCAVCSDYASGYHYGWSCEGCKAFF 120

174 KRSIQGHNDYICPATNOCTIDKNRKSCQACRLKCYEVGMVKGSRERCGYLVRRQR 233
Db 121 KRSIQGHNDYICPATNOCTIDKNRKSCQACRLKCYEVGMVKGSRERCGYLVRRQR 180

234 SADSOLHCAGKAKSGGHPAVRELLDALSPEOLVLTLEAEPPHVLISRPAFTFAS 293
Db 181 SADSOLHCAGKAKSGGHPAVRELLDALSPEOLVLTLEAEPPHVLISRPAFTFAS 240

294 MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLWNRSIDHPGK 353
Db 241 MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLWNRSIDHPGK 300

354 LIPADVLDRDEGKCVGILEIFDMLLATTSRFRELKLOHKEYLCVKAMILLNSSMYPL 413
Db 301 LIPADVLDRDEGKCVGILEIFDMLLATTSRFRELKLOHKEYLCVKAMILLNSSMYPL 360

414 VTATQDADSSRKLAHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHVRHASKGM 473
Db 361 VTATQDADSSRKLAHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHVRHASKGM 420

474 EHLNMMCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEGSONFQSQ 530
Db 421 EHLNMMCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEGSONFQSQ 477

RESULT 7
US-08-836-620A-2
Sequence 2, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORGANISM: Rattus rattus
US-08-836-620A-2

Query Match 81.7%; Score 2291; DB 2; Length 485;
Best Local Similarity 88.7%; Pred. No. 1.5e-236;
Matches 430; Conservative 23; Mismatches 32; Indels 0; Gaps 0;

46 MTFYSPAVMYIPSNVTNLEGGPGRQTSPNVLPPTGHLSPVVRQLSHLYAEPOKS 105
Db 1 MTFYSPAVMYIPSNVTNLEGGPGRQTSPNVLPPTGHLSPVVRQLSHLYAEPOKS 60

106 PWCEARSLREHTLPVNRRETLKRVSGNRKASPTVPGSKRDAHFCAVCSDYASGYHYGWS 165
Db 61 PWCEARSLREHTLPVNRRETLKRVSGNRKASPTVPGSKRDAHFCAVCSDYASGYHYGWS 120

166 CEGCKAFFKRSIQGHNDYICPATNOCTIDKNRKSCQACRLKCYEVGMVKGSRERCG 225
Db 121 CEGCKAFFKRSIQGHNDYICPATNOCTIDKNRKSCQACRLKCYEVGMVKGSRERCG 180

226 YRLVRRORSADQLHCAGKAKSGGHPAVRELLDALSPEOLVLTLEAEPPHVLISR 285
Db 181 YRLVRRORSADQLHCAGKAKSGGHPAVRELLDALSPEOLVLTLEAEPPHVLISR 240

286 SAPFTFASMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLW 345
Db 241 SAPFTFASMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLW 300

346 RSDHDPGLIFAPDVLDRDEGKCVGILEIFDMLLATTSRFRELKLOHKEYLCVKAMIL 405
Db 301 RSDHDPGLIFAPDVLDRDEGKCVGILEIFDMLLATTSRFRELKLOHKEYLCVKAMIL 360

406 LNSSMYPLVATQDADSSRKLAHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHV 465
Db 361 LNSSMYPLVATQDADSSRKLAHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHV 420

466 RHASNKGMEHLNMMCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEGSO 525
Db 421 RHASNKGMEHLNMMCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEGSO 480

526 NPOSQ 530
481 NLQSQ 485

RESULT 8
US-08-836-620A-13
Sequence 13, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor

Patent No. 6680368
GENERAL INFORMATION:
APPLICANT: Mosselman, Sietse
APPLICANT: Dijkema, Rein
TITLE OF INVENTION: No. 6680368el Estrogen Receptor
FILE REFERENCE: O/96193 US/DI
CURRENT APPLICATION NUMBER: US/09/608,088
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 08/826,361
PRIOR FILING DATE: 1997-03-26
PRIOR APPLICATION NUMBER: EP 96203284.3
PRIOR FILING DATE: 1996-11-22
PRIOR APPLICATION NUMBER: EP 96200820.7
PRIOR FILING DATE: 1996-03-26
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent in version 3.0
SEQ ID NO 5
LENGTH: 477
TYPE: PRT
ORGANISM: Homo sapiens
US-09-608-088-5

Query Match 89.9%; Score 2522; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.5e-261;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

54 MNYISPSNVNLEGGSGRQTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPKCRARSL 113
Db 1 MNYISPSNVNLEGGSGRQTSPNVLPPTGHLSPVVRQLSHLYAEPOKSPKCRARSL 60

114 EHTLPVNRRETLKRVSGNRKASPTVPGSKRDAHFCAVCSDYASGYHYGWSCEGCKAFF 173
Db 61 EHTLPVNRRETLKRVSGNRKASPTVPGSKRDAHFCAVCSDYASGYHYGWSCEGCKAFF 120

174 KRSIQGHNDYICPATNOCTIDKNRKSCQACRLKCYEVGMVKGSRERCGYLVRRQR 233
Db 121 KRSIQGHNDYICPATNOCTIDKNRKSCQACRLKCYEVGMVKGSRERCGYLVRRQR 180

234 SADSOLHCAGKAKSGGHPAVRELLDALSPEOLVLTLEAEPPHVLISRPAFTFAS 293
Db 181 SADSOLHCAGKAKSGGHPAVRELLDALSPEOLVLTLEAEPPHVLISRPAFTFAS 240

294 MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLWNRSIDHPGK 353
Db 241 MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESQMEVLMGLWNRSIDHPGK 300

354 LIPADVLDRDEGKCVGILEIFDMLLATTSRFRELKLOHKEYLCVKAMILLNSSMYPL 413
Db 301 LIPADVLDRDEGKCVGILEIFDMLLATTSRFRELKLOHKEYLCVKAMILLNSSMYPL 360

414 VTATQDADSSRKLAHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHVRHASKGM 473
Db 361 VTATQDADSSRKLAHLNAVTDALVWVIKSGISSQQSMRLANLMLLSHVRHASKGM 420

474 EHLNMMCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEGSONFQSQ 530
Db 421 EHLNMMCKNVVYVDLLEMLNARVLGCKSSITGSECSPAEDSKSKEGSONFQSQ 477

RESULT 7
US-08-836-620A-2
Sequence 2, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-836-620A-13

Query Match 81.5%; Score 2286; DB 2; Length 484;
Best Local Similarity 88.6%; Pred. No. 5.3e-236;
Matches 429; Conservative 23; Mismatches 32; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 46 | MTFYSPAVMNYSPSNVTNLEGGPGGRTTSPNVLPWTPGHLSPVVRQLSHLYAEPOKS | 105 |
| Db | 1 | MTFYSPAVMNYSPSGSTSLNDGGFVRLSTSPNVLPWTPGHLSPVVRQLSHLYAEPOKS | 60 |
| Qy | 106 | PWCEARSLHTLPVNRRTLKRVSGNRCASPVTPGSKRDAHFCVCSYASGYHYGWS | 165 |
| Db | 61 | PWCEARSLHTLPVNRRTLKRVSGNRCASPVTPGSKRDAHFCVCSYASGYHYGWS | 120 |
| Qy | 166 | CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVMVKCGSRRCG | 225 |
| Db | 121 | CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVMVKCGSRRCG | 180 |
| Qy | 226 | YRLVRQRSADEQLHCAGKAGSGGHAPRVRELLDALSPQLVLTLLAEPPHVLISRP | 285 |
| Db | 181 | YRLVRQRSADEQLHCAGKAGSGGHAPRVRELLDALSPQLVLTLLAEPPHVLISRP | 240 |
| Qy | 286 | SAPFTEASMMSLTKLADKELVHMIWAKKIPGVFVLSLFDQVRLLESQWVLMGLMW | 345 |
| Db | 241 | SMPFTEASMMSLTKLADKELVHMIWAKKIPGVFVLSLFDQVRLLESQWVLMGLMW | 300 |
| Qy | 346 | RSIDHPGKLIAPDLVLDREKQVEGILEIFDMLLATTSPRELKQHKYLCVKAMIL | 405 |
| Db | 301 | RSIDHPGKLIAPDLVLDREKQVEGILEIFDMLLATTSPRELKQHKYLCVKAMIL | 360 |
| Qy | 406 | LNSMYPVLTATQDADSSRLKLAHLINAVTDALVWVIAKSGISSQQSMRLANLMLLSHV | 465 |
| Db | 361 | LNSMYPVLTATQDADSSRLKLAHLINAVTDALVWVIAKSGISSQQSMRLANLMLLSHV | 420 |
| Qy | 466 | RHASKNGEHLNKKCNVVPVYDILLMLNAHVLRGCKSSITGSECSPAEDSKSKEGSO | 525 |
| Db | 421 | RHASKNGEHLNKKCNVVPVYDILLMLNAHVLRGCKSSITGSECSPAEDSKSKEGSO | 480 |
| Qy | 526 | NPOS 529 | |
| Db | 481 | NLOS 484 | |

RESULT 9

US-08-836-620A-5
Sequence 5, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Vers on #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-836-620A-5

Query Match 80.8%; Score 2267; DB 2; Length 485;

Best Local Similarity 88.0%; Pred. No. 5.7e-234;
Matches 427; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 46 | MTFYSPAVMNYSPSNVTNLEGGPGGRTTSPNVLPWTPGHLSPVVRQLSHLYAEPOKS | 105 |
| Db | 1 | MTFYSPAVMNYSPSGSTSLNDGGFVRLSTSPNVLPWTPGHLSPVVRQLSHLYAEPOKS | 60 |
| Qy | 106 | PWCEARSLHTLPVNRRTLKRVSGNRCASPVTPGSKRDAHFCVCSYASGYHYGWS | 165 |
| Db | 61 | PWCEARSLHTLPVNRRTLKRVSGNRCASPVTPGSKRDAHFCVCSYASGYHYGWS | 120 |
| Qy | 166 | CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVMVKCGSRRCG | 225 |
| Db | 121 | CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKCYEVMVKCGSRRCG | 180 |
| Qy | 226 | YRLVRQRSADEQLHCAGKAGSGGHAPRVRELLDALSPQLVLTLLAEPPHVLISRP | 285 |
| Db | 181 | YRLVRQRSADEQLHCAGKAGSGGHAPRVRELLDALSPQLVLTLLAEPPHVLISRP | 240 |
| Qy | 286 | SAPFTEASMMSLTKLADKELVHMIWAKKIPGVFVLSLFDQVRLLESQWVLMGLMW | 345 |
| Db | 241 | SMPFTEASMMSLTKLADKELVHMIWAKKIPGVFVLSLFDQVRLLESQWVLMGLMW | 300 |
| Qy | 346 | RSIDHPGKLIAPDLVLDREKQVEGILEIFDMLLATTSPRELKQHKYLCVKAMIL | 405 |
| Db | 301 | RSIDHPGKLIAPDLVLDREKQVEGILEIFDMLLATTSPRELKQHKYLCVKAMIL | 360 |
| Qy | 406 | LNSMYPVLTATQDADSSRLKLAHLINAVTDALVWVIAKSGISSQQSMRLANLMLLSHV | 465 |
| Db | 361 | LNSMYPVLTATQDADSSRLKLAHLINAVTDALVWVIAKSGISSQQSMRLANLMLLSHV | 420 |
| Qy | 466 | RHASKNGEHLNKKCNVVPVYDILLMLNAHVLRGCKSSITGSECSPAEDSKSKEGSO | 525 |

Db 421 RHISNKGHEHLSNKKNNVVPVYDILLEMLNAHTLRYKSSISGSGCCSTEDSKSKEGSO 480

Qy 526 NPOSO 530

Db 481 NLQSO 485

RESULT 10

US-08-836-620A-14

; Sequence 14, Application US/08836620A

; Patent No. 5958710

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Orphan receptor

; NUMBER OF SEQUENCES: 19

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/836,620A

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP96/03833

; FILING DATE:

; APPLICATION NUMBER: GB 9518272.1

; FILING DATE: 08-SEP-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9605550.4

; FILING DATE: 15-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9607532.0

; FILING DATE: 11-APR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9609576.5

; FILING DATE: 08-MAY-1996

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 484 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; ORIGINAL SOURCE:

; ORGANISM: Mus musculus

US-08-836-620A-14

Query Match 80.6%; Score 2262; DB 2; Length 484;

Best Local Similarity 88.0%; Pred. No. 2e-233;

Matches 426; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

Qy 46 MTFYSPAVMYSIPSNVTNLEGGPGRTTSPNVLMPPTGHLSPVLVHRLSHLYAEPQKS 105

Db 1 MAFYSPAVMYSIPSNVTNLEGGPGRTTSPNVLMPPTGHLSPVLVHRLSHLYAEPQKS 60

Qy 106 PWCEARSLEHTLPVNRRTLKRKYSNRCASPTGSKRDAHFCAVCSYASGYHYGVMS 165

Db 61 PWCEARSLEHTLPVNRRTLKRKYGSGCASPTGSKRDAHFCAVCSYASGYHYGVMS 120

Qy 166 CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVKCGSRRCG 225

Db 121 CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVKCGSRRCG 180

Qy 226 YRLVRQRSDAEOLHCHAGKAKRSQGHAPRVRELLDALSPEQLVLTLEAEPHVLISRP 285

Db 181 YRLVRQRSDAEOLHCHAGKAKRSQGHAPRVRELLDALSPEQLVLTLEAEPHVLISRP 240

Qy 286 SAEFTASMMSTLTKADKELVHMISWAKKIPGVFELSFDQVRLLESQWMEVLMGLMW 345

Db 241 SAEFTASMMSTLTKADKELVHMISWAKKIPGVFELSFDQVRLLESQWMEVLMGLMW 300

Qy 346 RSIDHPKGLIFAPDLVLDREDEKCVGEILEIFDMLLATTSRRELKLOHKEYLCVKAMIL 405

Db 301 RSIDHPKGLIFAPDLVLDREDEKCVGEILEIFDMLLATTSRRELKLOHKEYLCVKAMIL 360

Qy 406 LNSMYPLVATQADSSRLAHLNAVTDALVWVIKSGISGSGCCSTEDSKSKEGSO 465

Db 361 LNSMYPLVATQADSSRLAHLNAVTDALVWVIKSGISGSGCCSTEDSKSKEGSO 420

Qy 466 RHASNKGHEHLSNKKNNVVPVYDILLEMLNAHTLRYKSSISGSGCCSTEDSKSKEGSO 525

Db 421 RHISNKGHEHLSNKKNNVVPVYDILLEMLNAHTLRYKSSISGSGCCSTEDSKSKEGSO 480

Qy 526 NPOSO 529

Db 481 NLQSO 484

RESULT 11

US-09-608-088-6

; Sequence 6, Application US/09608088

; Patent No. 6680368

; GENERAL INFORMATION:

; APPLICANT: Mosselman, Sietse

; APPLICANT: Dijkema, Rein

; TITLE OF INVENTION: No. 6680368e1 Estrogen Receptor

; FILE REFERENCE: 0/96193 US/D1

; CURRENT APPLICATION NUMBER: US/09/608,088

; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 08/826,361

; PRIOR FILING DATE: 1997-03-26

; PRIOR APPLICATION NUMBER: EP 96203284.3

; PRIOR FILING DATE: 1996-11-22

; PRIOR APPLICATION NUMBER: EP 96200820.7

; PRIOR FILING DATE: 1996-03-26

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 6

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-608-088-6

Query Match 78.4%; Score 2198; DB 4; Length 416;

Best Local Similarity 100.0%; Pred. No. 1.1e-226;

Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 MNYSPSNVTNLEGGPGRTTSPNVLMPPTGHLSPVLVHRLSHLYAEPQKSFWCEARSL 113

Db 1 MNYSPSNVTNLEGGPGRTTSPNVLMPPTGHLSPVLVHRLSHLYAEPQKSFWCEARSL 60

Qy 114 EHTLPVNRRTLKRKYSNRCASPTGSKRDAHFCAVCSYASGYHYGVMSCEGCKAFF 173

Db 61 EHTLPVNRRTLKRKYSNRCASPTGSKRDAHFCAVCSYASGYHYGVMSCEGCKAFF 120

Qy 174 KRSTQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVKCGSRRCGVLVRRQR 233

Db 121 KRSTQGHNDYICPATNQCTIDKNRRKSCQACRLKCYEYGVKCGSRRCGVLVRRQR 180

Qy 234 SADEQLHCAGKAKRSQGHAPRVRELLDALSPEQLVLTLEAEPHVLISRPSPAPTEAS 293

Db 181 SADEQLHCAGKAKRSQGHAPRVRELLDALSPEQLVLTLEAEPHVLISRPSPAPTEAS 240

Qy 294 MMSLTKLADKELVHMISWAKKIPGVFELSFDQVRLLESQWMEVLMGLMWRSIDHPCK 353

Db 241 MMSLTKLADKELVHMISWAKKIPGVFELSFDQVRLLESQWMEVLMGLMWRSIDHPCK 300

Qy 354 LIAPDLVLDREDEKCVGEILEIFDMLLATTSRRELKLOHKEYLCVKAMILNLSMYP 413

Db 301 LIAPDLVLDREDEKCVGEILEIFDMLLATTSRRELKLOHKEYLCVKAMILNLSMYP 360

Qy 414 VTATQADSSRLAHLNAVTDALVWVIKSGISGSGCCSTEDSKSKEGSO 468

Db 361 VTATQADSSRLAHLNAVTDALVWVIKSGISGSGCCSTEDSKSKEGSO 415

RESULT 12

US-09-608-088-21
; Sequence 21, Application US/09608088
; Patent No. 6680368
; GENERAL INFORMATION:
; APPLICANT: Mosselman, Sietse
; APPLICANT: Dijkema, Rein
; TITLE OF INVENTION: No. 6680368e1 Estrogen Receptor
; FILE REFERENCE: O/96193 US/D1
; CURRENT APPLICATION NUMBER: US/09/608,088
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 08/826,361
; PRIOR FILING DATE: 1997-03-26
; PRIOR APPLICATION NUMBER: EP 96203284.3
; PRIOR FILING DATE: 1996-11-22
; PRIOR APPLICATION NUMBER: EP 96200820.7
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 21
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-088-21

Query Match 78.4%; Score 2198; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.1e-226;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 MYSIPSNVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRQSHLYAEQKSPWCEARSL 113
DB 1 MYSIPSNVTNLEGGPGROTTSPNVLWPTPGHLSPLVVRQSHLYAEQKSPWCEARSL 60

QY 114 EHTLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSYASGYHYGWSCEGCKAFF 173
DB 61 EHTLPVNRRLTKRKVSGNRCASPVTPGSKRDHAFCAVCSYASGYHYGWSCEGCKAFF 120

QY 174 KRSIQGHNDYICPATNOCTIDKRRKSCQACRLKCYEVMKCGSRRCGVLVRROR 233
DB 121 KRSIQGHNDYICPATNOCTIDKRRKSCQACRLKCYEVMKCGSRRCGVLVRROR 180

QY 234 SADEQLHCAGKAKRSGGHAPRVRELLLDALSPQLVLTLEAPPVHLISRPSAPTEAS 293
DB 181 SADEQLHCAGKAKRSGGHAPRVRELLLDALSPQLVLTLEAPPVHLISRPSAPTEAS 240

QY 294 MMMSLTKLADKELVHMISWAKKIPGVFELSFPQVRLLESQWVLMGLMWSRIDHPCK 353
DB 241 MMMSLTKLADKELVHMISWAKKIPGVFELSFPQVRLLESQWVLMGLMWSRIDHPCK 300

QY 354 LIFAPDLVLRDRGKCVGEILEIFDMLLATTSPRELKLQHKYLCVKAMILLNSSMYPL 413
DB 301 LIFAPDLVLRDRGKCVGEILEIFDMLLATTSPRELKLQHKYLCVKAMILLNSSMYPL 360

QY 414 VTATQDADSSRLKLAHLINAVTDALVWVIKSGISSQQQSRMLANLMLLSHVRHA 468
DB 361 VTATQDADSSRLKLAHLINAVTDALVWVIKSGISSQQQSRMLANLMLLSHVRHA 415

RESULT 13
US-08-836-620A-15
; Sequence 15, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT: Orphan receptor
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:

PRIOR APPLICATION DATA: PCT/EP96/01933
; FILING DATE: GB 9518272.1
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-836-620A-15

Query Match 71.9%; Score 2017; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.5e-207;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 LSPLVVRQLSHLYAEQKSPWCEARSLHTLPVNRRLTKRKVSGNRCASPVTPGSKRD 145
DB 2 LSPLVVRQLSHLYAEQKSPWCEARSLHTLPVNRRLTKRKVSGNRCASPVTPGSKRD 61

QY 146 AHFCAVCSDYASGYHYGWSCEGCKAPFKRSIQGHNDYICPATNOCTIDKRRKSCQACR 205
DB 62 AHFCAVCSDYASGYHYGWSCEGCKAPFKRSIQGHNDYICPATNOCTIDKRRKSCQACR 121

QY 206 LRKCYEVMKCGSRRCGVLVRRORSADEQLHCAGKAKRSGGHAPRVRELLLDALSP 265
DB 122 LRKCYEVMKCGSRRCGVLVRRORSADEQLHCAGKAKRSGGHAPRVRELLLDALSP 181

QY 266 BOLVLTLEAPPVHLISRPSAPTEASMMMSLTKLADKELVHMISWAKKIPGVFELSFP 325
DB 182 BOLVLTLEAPPVHLISRPSAPTEASMMMSLTKLADKELVHMISWAKKIPGVFELSFP 241

QY 326 DOVRLLESQWVLMGLMWSRIDHPGKLIIFAPDLVLRDRGKCVGEILEIFDMLLATTSP 385
DB 242 DOVRLLESQWVLMGLMWSRIDHPGKLIIFAPDLVLRDRGKCVGEILEIFDMLLATTSP 301

QY 386 RFRELKLQHKYLCVKAMILLNSSMYPLVTATQDADSSRLKLAHLINAVTDALVWVIKSG 445
DB 302 RFRELKLQHKYLCVKAMILLNSSMYPLVTATQDADSSRLKLAHLINAVTDALVWVIKSG 361

QY 446 ISSQQQSRMLANLMLLSHVRHA 468
DB 362 ISSQQQSRMLANLMLLSHVRHA 384

RESULT 14
US-08-764-870-12
; Sequence 12, Application US/08764870
; Patent No. 6236946
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Thomas S
; APPLICANT: Baxter, John D
; APPLICANT: Fletcher, Robert J
; APPLICANT: Wagner, Richard L
; APPLICANT: Kushner, Peter J
; APPLICANT: Aprelitti, James W
; APPLICANT: West, Brian
; TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
; TITLE OF INVENTION: Binding Domains
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward

STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UCAL-246/0105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)843-5000
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-764-870-12

Query Match 44.0%; Score 1233.5; DB 3; Length 595;
Best Local Similarity 48.4%; Pred. No. 5.2e-123;
Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;

Qy 5 NSPSSLSNSPSSYNSCSQSLPLEH--GSIIYIPSS--YVDSHHEYPAMTFYSPAVMYNYSIPS 60
Db 21 NELEPLNRP-----QKIIPLERPLGEVLDSSKPAVNYPEGAAYEFNAANAQAQVYG 74

Qy 61 NVTNLGGGGRQ-----TTSNVLWPTPGHLSP-LVVRQLSHLYAE 101
Db 75 Q-TGLPYGSGEAAAFSGNLGFPPLNSVSPSLMLLHPPLQSPFLQHGQOVPYLE 133

Qy 102 PQKSPWC--EARSLEHTLPVNRKYLKRVSGNRCASPVYTGPG-----SKDAHFCAVCS 154
Db 134 NEPSGYTVREAGPPAFYRP---NSDNRROGGRERLASTNDKGSMAVESAKETRYCAVCND 190

Qy 155 YASGYHYGVNSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKRCYEVGM 214
Db 191 YASGYHYGVNSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKRCYEVGM 250

Qy 215 VKGSRRERCYRLVRQRSADEQLHCAGKAKRSGGHA PRV-----EL 258
Db 251 MKGGIRKDRRGGRMLKHKRQDD-----GEGRGVSGAGDMRAANLWPSPLMIKRSKNS 305

Qy 259 LLDALSPQVLTLLEAPPPHVLISR--PSAPFTEASMMMSLTKLADKELVHMSWAKKI 316
Db 306 LALSITADQWYSLDADAPP-ILYSEYDPTFPFSEASMMGLTTLADRELVHMLNWAQV 364

Qy 317 FGVVELSLFDQVRLLESCEMVEMLMWRSIDHPGKLIIPAPDLVDRDRCKVEGILEI 376
Db 365 FGFVDLTLDQVHLECAWLBIIMGLVWRSMHPGKLLFAPNLLDRNQGCKVEGMVEI 424

Qy 377 FDMILLATTSRRELKLOHKEYLVCKAMILLNSSMYPLVAT- QDADSSRLKLAHLNATVD 435
Db 425 FDMILLATTSRFRMNLQGEFVCLKSIILLNSGYTTFLLSTLKSLEEKDHRVLDKIID 484

Qy 436 ALVWVIAKSGISSQOSQSMELANILMLLSHVHRASNKGMHEHLLNMKCNVVPVYDILLEM 495
Db 485 TLHLAKAGLTIQOHOHQRLAQLLLSHIRWSNKGMHEHLLNMKCNVVPVYDILLEM 544

Qy 496 NAHVL 500
Db 545 DAHRL 549

RESULT 15
US-08-980-115-12
Sequence 12, Application US/08980115
Patent No. 6266622
GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxter, John D.
APPLICANT: Fletterick, Robert J.
APPLICANT: Wagner, Richard L.
APPLICANT: Kushner, Peter J.
APPLICANT: Apriletti, James W.
APPLICANT: West, Brian L.
APPLICANT: Shiau, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
FILE REFERENCE: UCAL-246/0205
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 60/008,606
EARLIER FILING DATE: 1995-12-14
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 595
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (287)...(549)
OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-12

Query Match 44.0%; Score 1233.5; DB 3; Length 595;
Best Local Similarity 48.4%; Pred. No. 5.2e-123;
Matches 264; Conservative 88; Mismatches 128; Indels 65; Gaps 14;

Qy 5 NSPSSLSNSPSSYNSCSQSLPLEH--GSIIYIPSS--YVDSHHEYPAMTFYSPAVMYNYSIPS 60
Db 21 NELEPLNRP-----QKIIPLERPLGEVLDSSKPAVNYPEGAAYEFNAANAQAQVYG 74

Qy 61 NVTNLGGGGRQ-----TTSNVLWPTPGHLSP-LVVRQLSHLYAE 101
Db 75 Q-TGLPYGSGEAAAFSGNLGFPPLNSVSPSLMLLHPPLQSPFLQHGQOVPYLE 133

Qy 102 PQKSPWC--EARSLEHTLPVNRKYLKRVSGNRCASPVYTGPG-----SKDAHFCAVCS 154
Db 134 NEPSGYTVREAGPPAFYRP---NSDNRROGGRERLASTNDKGSMAVESAKETRYCAVCND 190

Qy 155 YASGYHYGVNSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKRCYEVGM 214
Db 191 YASGYHYGVNSCEGCKAPFKRSIQGHNDYICPATNQCTIDKNRKSQAACRLKRCYEVGM 250

Qy 215 VKGSRRERCYRLVRQRSADEQLHCAGKAKRSGGHA PRV-----EL 258
Db 251 MKGGIRKDRRGGRMLKHKRQDD-----GEGRGVSGAGDMRAANLWPSPLMIKRSKNS 305

Qy 259 LLDALSPQVLTLLEAPPPHVLISR--PSAPFTEASMMMSLTKLADKELVHMSWAKKI 316

| | | | |
|----|-----|--|-----|
| Db | 306 | LALSLTADQWVSALLDAEPP-ILYSEYDTPFPSEASMGLLTNTLADRELVEHINWAKRV | 364 |
| Qy | 317 | PGFVELSLFDQVRLLESQWNEVLAMGLMWRSDHPGKLIIPAPDLVLDREBKCVEGILEI | 376 |
| Db | 365 | PGFVDTLTHDQVHLLECAWLEILMIGLVWRSMHPGKLIIPAPNLLDRNQCKVEGWVEI | 424 |
| Qy | 377 | FDMLATTSSREKLQKHKEYLCVKAMILLNSSNYPLVATAT-ODADSSRKLAHLNAVTD | 435 |
| Db | 425 | FDMLLATSSRFMMNLQGEFVCLKSIIILLNSGVYTFLSSTLKSLEBKDHHRVLDKITD | 484 |
| Qy | 436 | ALVWVIKSGISSQQQSMRLANLMLLSHVYRHSNKGMEHLNNKCKNVVVPVYDILLEML | 495 |
| Db | 485 | TLJHLNAKAGLTLQQQHORIQAQLLLIILSHIRHMSNKGMEHLYSMKCKNVVPLYDILLEML | 544 |
| Qy | 496 | NAVVL 500 | |
| Db | 545 | DAHRL 549 | |

Search completed: June 20, 2004, 10:39:47
Job time : 25 secs